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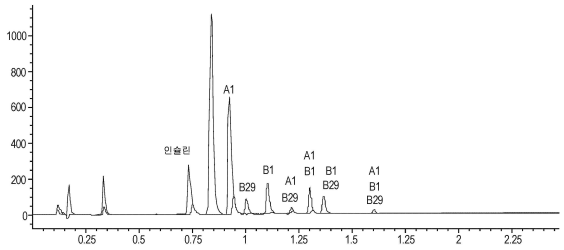
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(54) 발명의 명칭 **페니실린 G 아실라제**

(57) 요 약

본 발명은 개선된 특성을 가지는 조작된 페니실린 G 아실라제(PGA) 효소, 상기 효소를 코딩하는 폴리뉴클레오티드, 상기 효소를 포함하는 조성물, 및 상기 효소를 사용하는 방법을 제공한다.

대 표 도



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명 세 서

청구범위

청구항 1

서열 번호: 1036과 적어도 95% 동일한 폴리펩티드 서열을 가지는 조작된 페니실린 G 아실라제로서, 상기 페니실린 G 아실라제는 서열 번호: 1036의 서열과 비교하여 X2 위치에 류신 잔기를 포함하는 것인 조작된 페니실린 G 아실라제.

청구항 2

제1항에 있어서, 상기 페니실린 G 아실라제는 서열 번호: 1194를 포함하는 것인 조작된 페니실린 G 아실라제.

청구항 3

제1항에 있어서, 상기 페니실린 G 아실라제는 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 생산할 수 있는 것인 조작된 페니실린 G 아실라제.

청구항 4

제1항에 있어서, 상기 페니실린 G 아실라제는 서열 번호: 1194-1254 중 짝수 번호의 서열로부터 선택된 폴리펩티드 서열을 포함하는 것인 조작된 페니실린 G 아실라제.

청구항 5

삭제

청구항 6

제1항의 조작된 페니실린 G 아실라제를 코딩하는 조작된 폴리뉴클레오티드.

청구항 7

제6항에 있어서, 상기 조작된 폴리뉴클레오티드는 서열 번호: 1193-1253 중 홀수 번호의 서열로부터 선택된 폴리뉴클레오티드 서열을 포함하는 것인 조작된 폴리뉴클레오티드.

청구항 8

제6항에 있어서, 상기 조작된 폴리뉴클레오티드는 서열 번호: 1193을 포함하는 조작된 폴리뉴클레오티드.

청구항 9

i) 제1항의 조작된 페니실린 G 아실라제 및/또는 상기 조작된 페니실린 G 아실라제를 포함하는 조성물, 및 A1/B1/B29 트리-페닐 아세테이트 보호기를 포함하는 인슐린을 제공하는 단계; 및 ii) 상기 조작된 페니실린 G 아실라제가 상기 인슐린으로부터 A1, B1 및/또는 B29 트리-페닐 아세테이트 보호기를 제거하여 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 제조하도록 하는 조건하에서, 상기 조작된 페니실린 G 아실라제를 A1/B1/B29 트리-페닐 아세테이트 보호기를 포함하는 상기 인슐린에 노출시키는 단계를 포함하는, 페닐 아세테이트 단일 보호된 인슐린을 제조하는 방법.

청구항 10

제9항에 있어서, 상기 페니실린 G 아실라제는 상기 인슐린의 A1 트리-페닐 아세테이트 보호기를 제거하는 것인 방법.

청구항 11

제9항에 있어서, 상기 페니실린 G 아실라제는 상기 인슐린의 B1 트리-페닐 아세테이트 보호기를 제거하는 것인 방법.

청구항 12

제9항에 있어서, 상기 페니실린 G 아실라제는 상기 인슐린의 B29 트리-페닐 아세테이트 보호기를 제거하는 것인 방법.

청구항 13

제9항에 있어서, 상기 페니실린 G 아실라제는 상기 인슐린의 A1, B1, 및 B29 트리-페닐 아세테이트 보호기를 제거하는 것인 방법.

청구항 14

제9항에 있어서, 상기 조작된 페니실린 G 아실라제는, 서열 번호: 2의 폴리펩티드에 의한 페닐 아세테이트 단일 보호된 인슐린의 생산과 비교하였을 때, 페닐 아세테이트 단일 보호된 인슐린을 90% 초과로 생산하는 것인 방법.

청구항 15

제1항에 있어서, 상기 페니실린 G 아실라제는 서열 번호: 1220을 포함하는 것인 조작된 페니실린 G 아실라제.

청구항 16

삭제

청구항 17

삭제

청구항 18

삭제

청구항 19

삭제

청구항 20

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청구항 46

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청구항 47

삭제

청구항 48

삭제

청구항 49

삭제

발명의 설명

기 술 분 야

[0001] 본 출원은 2016년 5월 6일 출원된 미국 가특허 출원 제62/332,103호에 대한 우선권을 주장하며, 상기 출원은 그 전문이 모든 목적을 위해 본원에서 참조로 포함된다.

[0002] **본 발명의 분야**

[0003] 본 발명은 조작된 페니실린 G 아실라제(PGA: penicillin G acylase) 효소, 상기 효소를 코딩하는 폴리뉴클레오티드, 상기 효소를 포함하는 조성물, 및 조작된 PGA 효소를 사용하는 방법을 제공한다.

[0004] **서열 목록, 표 또는 컴퓨터 프로그램에 관한 참조**

[0005] 파일명이 "CX2-154WO1_ST25.txt"이고, 작성일이 2017년 5월 5일이며, 크기가 8,962 킬로바이트 인 서열 목록의 공식 사본은 ASCII 포맷된 텍스트 파일로서 EFS-웹을 통해 본 명세서와 함께 동시에 제출된 것이다. EFS-웹을 통해 제출된 서열 목록은 본 명세서의 일부이며, 이는 그 전문이 본원에서 참조로 포함된다.

배 경 기 술

[0006] 페니실린 G 아실라제(PGA)(페니실린 아미다제, EC 3.5.1.11)는 페니실린 G(벤질페니실린) 측쇄의 아미드 결합의 절단을 촉매화한다. 상기 효소는 6-아미노-페니실란산(6-APA: 6-amino-penicillanic acid) 및 페닐-아세트산(PAA: phenyl-acetic acid)의 제조에서 상업적으로 사용된다. 6-APA는 반합성 β 락탐 항생제, 예컨대, 아목시실린, 암피실린 및 세팔렉신의 산업적 생산에서 핵심 화합물이다. 자연적으로 발생된 PGA 효소는 상업적 프로세스에서 불안정성을 보이는 바, 상업적 적용을 위해서는 고체 기판 상에의 고정화가 요구된다. PGA는 다양한 지지체에 공유적으로 결합되었고, PGA 고정화된 시스템은 순수한 광학 이성질체의 합성을 위한 유용한 도구로서 보고되었다. 그러나, 고체 표면에의 부착은 예컨대, 활성 및/또는 선택성 감소, 및 용질 접근의 제한과 같이, 효소 특성을 손상시킨다. 더욱이, 비록 고체 기판에의 부착을 통해 효소가 포획될 수 있고, 추가의 프로세싱 사이클에서 재사용이 가능하지만, 효소의 안정성은 그 적용이 제한될 수 있는 정도이다. 페니실린 G에서 6-APA로의 PGA에 의한 효소적 촉매 작용은 위치특이적이고(락탐 아미드 결합은 절단하지 않음), 입체특이적이다. 6-APA 생산은 아마도 의약 생산에서 효소적 촉매 작용을 최대로 이용하는 것으로 여겨진다. 펜아세틸 모이어티와 회합된, PGA의 효소 활성은 알콜 뿐만 아니라, 1급 아민의 매우 다양한 펜아세틸 유도체의 입체특이적 가수분해를

가능하게 한다.

발명의 내용

[0007] 본 발명은 조작된 페니실린 G 아실라제(PGA) 효소, 상기 효소를 코딩하는 폴리뉴클레오티드, 상기 효소를 포함하는 조성물, 및 조작된 PGA 효소를 사용하는 방법을 제공한다.

[0008] 본 발명은 유리 인슐린의 A1, B1 또는 B29 위치에 보호기를 부가함으로써, 또는 A1/B1/B29 삼중 보호된 인슐린으로부터 보호기를 제거함으로써 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 생산할 수 있는 조작된 페니실린 G 아실라제를 제공한다. 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 약 85%, 약 86%, 약 87%, 약 88%, 약 89%, 약 90%, 약 91%, 약 92%, 약 93%, 약 94%, 약 95%, 약 96%, 약 97%, 약 98%, 약 99% 또는 그 이상 동일하다. 일부 실시양태에서, 본 발명은 인슐린으로부터 A1, B1, 또는 B29 트리-페닐 아세테이트 보호기를 제거하여 디-페닐 아세테이트 보호된 인슐린을 생산할 수 있는 조작된 페니실린 G 아실라제로서, 여기서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 것인, 조작된 페니실린 G 아실라제를 제공한다. 일부 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1 트리-페닐 아세테이트 보호기를 제거하는 반면, 일부 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 B1 트리-페닐 아세테이트 보호기를 제거하고, 또 다른 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 B29 트리-페닐 아세테이트 보호기를 제거한다. 일부 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1, B1, 및 B29 트리-페닐 아세테이트 보호기를 제거한다. 일부 추가의 실시양태에서, 조작된 페니실린 G 아실라제는, 서열 번호: 2의 폴리펩티드에 의한 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린의 생산과 비교하였을 때, 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 초과 또는 그 이상으로 생산한다.

[0009] 일부 추가의 실시양태에서, 본 발명은 인슐린으로부터 A1/B1/B29 트리-페닐 아세테이트 보호기를 제거함으로써 유리 인슐린을 생산할 수 있는 조작된 페니실린 G 아실라제로서, 여기서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288를 포함하는 것인, 조작된 페니실린 G 아실라제를 제공한다. 일부 추가의 실시양태에서, 페니실린 G 아실라제는 표 5.1, 6.1, 7.1, 8.1, 8.2, 9,1, 10.1, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 및/또는 12.7에 제공된 바와 같은 페니실린 G 변이체 중 적어도 하나의 돌연변이를 포함한다. 일부 실시양태에서, 본 발명은 표 5.1, 6.1, 7.1, 8.1, 8.2, 9,1, 10.1, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 및/또는 12.7에 기재된 적어도 하나의 서열과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 서열을 포함하는 조작된 페니실린 G 아실라제를 제공한다. 일부 실시양태에서, 페니실린 G 아실라제는 표 5.1, 6.1, 7.1, 8.1, 8.2, 9,1, 10.1, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 및/또는 12.7에 제공된 변이체를 포함한다.

[0010] 본 발명은 또한, 서열 번호: 8과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 27, 27;28;71;74;547, 27;71;74;484;547;584;697, 71;74, 129, 253, 254, 256, 348, 352, 372, 373, 374, 380, 380;457, 386;390, 386;390, 386, 387;390, 451, 457, 467, 470, 474, 616, 623, 704, 706, 및 708로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 8을 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0011] 본 발명은 또한, 서열 번호: 14와 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 9, 9;103;119;131;233;312;324;432;444;494, 9;103;119;131;324;432;494;646, 9;103;119;131;233;269;304;444;494;646, 9;103;119;131;304;324;432;444;494;646, 9;103;119;233;646, 9;103;119;494, 9;103;233;312;646, 9;103;233;432;646, 9;103;233;494, 9;103;269;304;324;494;646, 9;103;304;432;444;646, 9;119;131;233, 9;119;131;233;304;444;646, 9;119;131;233;494;646, 9;119;131;233;494;661, 9;119;131;312;444;646, 9;119;131;432;444;646, 9;119;233;269;273;304;312;432;444;646, 9;119;233;494;646, 9;119;304;444;494;646, 9;131;233;269;273;312;432;444;646, 9;233;273;304;494;646, 9;233;304;494;646, 9;233;312;432;646, 9;233;494;646, 9;312;444;646, 9;432;444;494;646, 9;494;646, 28;374;380, 103;119;131;233;273;304;324;432;444;494;646, 103;119;131;233;304;312;432;494;646;661, 103;119;131;269;312;494;646, 103;119;233, 103;119;233;273;432, 103;119;233;304;646,

103;119;233;312;646, 103;119;494;646;661, 103;119;646, 103;131;233;304;324;444;646, 103;131;269;273;444;646, 103;233;273;312;324;432;444;646, 103;233;273;312;432;444;646, 103;269;273;444;646, 103;273;304;324;444;494, 103;312;444;646, 103;444;494;646, 119;131;444;646;661, 119;131;494, 119;131;646, 119;131;304;432;444;646;661, 119;131;444, 119;233;304;312;324;432;444;646, 119;233;304;646, 119;233;312, 119;233;646, 119;269;273;312;324;494;646, 119;269;273;312;432;444;646, 119;273;324;444;494;646, 119;312;444;646, 119;432;444;646, 129;254;348;457;704, 129;348, 129;348;467;470;704;708, 129;348;470;623;704;706, 129;348;470;623;704;706;708, 129;380;470, 129;457;470;474, 129;470,129;623, 131;233;273;646, 131;233;304;444, 131;233;432;646, 131;273;432;444;494;646, 185, 233;269;304;312;324;432;444;646, 253, 253;256, 253;256;352;373;374;616, 253;256;352;374;380;451, 253;256;374;451, 253;256;380;451;616, 253;352;374;616, 253;352;451;616, 253;373;451, 253;374;451, 253;374;451;623, 253;451, 253;451;457, 253;254;352;374;380, 253;256, 253;256;352;374;451, 253;256;352;380;451;616, 253;256;352;451, 253;256;352;374;380;451, 253;256;352;380, 253;256;373, 253;256;374;616, 253;256;380, 253;256;380;451;546;616, 253;352;373;374;451, 253;352;373;374;451;616, 253;352;374;616, 253;352;623, 253;373;374;451;616, 253;380, 254;255;352, 254;256;352;451, 254;256;373;374;380;451, 254;256;374, 254;256;374;451, 254;256;451, 254;352;380, 254;256;380;451;616, 254;352;380;451, 254;352;451, 254;373;374;380;451, 254;373;374;451, 254;374, 254;374;380, 254;380, 254;451, 254;616, 256;352;374, 256;352;380;451;616, 256;374;380;451;616, 256;374;616, 273;312;444;646, 304;312;444;646, 312;444;646, 312;646, 348, 348;372;470;623;708, 348;704;708, 352, 352;373;374;451, 352;373;380;451, 352;373;380;451;616, 352;373;451, 352;374, 352;374;380, 352;374;380;451;616, 352;374;451, 352;374;616, 352;380, 352;380;451, 352;380;451;616, 352;380;451;623, 352;380;616, 352;451, 352;451;616, 352;616, 372;457;470;623, 373;374, 373;374;451, 373;451, 373;616, 374, 374;380, 374;380;451, 374;380;451;623, 374;451, 374;451;616, 374;616, 374;623, 380, 380;451, 380;451;616, 380;451;623, 380;616, 380;616;623, 380;623, 415, 443, 444, 444;494, 444;646, 451, 451;616, 451;623, 457, 457;470, 457;704;708, 470;708, 492;493, 517, 560, 616, 623, 723, 및 748로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 14를 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0012] 본 발명은 또한, 서열 번호: 300과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 9;61;444, 9;168;185;517;560;748, 9;185;415, 9;185;415;443;444;517;723;748, 9;185;415;443;444;517;560, 9;185;415;443;444;517;748, 9;185;415;444;517;723;748, 9;185;415;444;517;748, 9;185;415;444;517;560, 9;185;415;444;517;560;723;748, 9;185;415;444, 9;185;415;444;560, 9;185;415;444;723;748, 9;185;415;444;517;560;723;748, 9;185;415;517;560, 9;185;415;517;723, 9;185;415;517;748, 9;185;415;748, 9;185;443;444;517;560, 9;185;443;444;723, 9;185;443;444;560;723, 9;185;443;444;517, 9;185;444, 9;185;444;517;560, 9;185;444;560;723, 9;185;444;560;748, 9;185;444;517;560, 9;185;444;517;560;723, 9;185;444;517;560;748, 9;185;444;517;723;748, 9;185;444;560, 9;185;444;723, 9;185;444;517;560;723, 9;185;517, 9;185;517;560;723;748, 9;185;748, 9;415;443;444;517;560, 9;415;443;444;517;748, 9;415;443;444;560;723;748, 9;415;443;444;517;560, 9;415;443;444;517;560;723, 9;415;443;444;517;748, 9;415;443;560, 9;415;443;560;723;748, 9;415;444, 9;415;444;517;560;748, 9;415;444;517, 9;415;444;517;560;723;748, 9;415;444;560;723;748, 9;415;444;723;748, 9;415;444;517, 9;415;444;517;560;723;748, 9;415;444;560;723, 9;415;444;517, 9;415;444;517;560;748, 9;415;444;517, 9;415;444;560, 9;415;444;560, 9;415;444;517;560;723, 9;415;444;560, 9;415;444;560;665;723;748, 9;415;444;723;748, 9;415;517, 9;415;517;560;723;748, 9;415;517;560;723;748, 9;415;517;560;748, 9;415;560, 9;415;748, 9;443;444;517;560;723, 9;443;444;560, 9;443;444;560;723;748, 9;443;444;517, 9;443;444;560;723, 9;443;444;517, 9;443;444;517;560, 9;443;444;517;748, 9;443;517;748, 9;443;723, 9;444;517;560, 9;444;560;723, 9;444;748, 9;444;517;560;723;748, 9;444;560, 9;444;560;723, 9;444;560;748, 9;444;560;748, 9;444;748, 9;444;517;560;723;748, 9;444;517, 9;444;517;560;723, 9;444;517;723, 9;444;560;748, 9;444;723, 9;444, 9;444;517;560, 9;517, 9;517;560;723, 9;517;560;748, 9;517;560;748, 9;517;723, 9;517;748, 9;560;723;748, 9;723, 103, 103;119, 103;119;129;254;256;348;494;646, 103;119;129;444;494, 103;119;254;348,103;119;254;348;444, 103;119;254;444, 103;119;256;348;444;494;646, 103;119;256;494, 103;119;348, 103;119;348;457,

103;119;348;457;494, 103;119;457, 103;119;494, 103;119;494;646, 103;129, 103;129;254;444;457;494, 103;129;256;348, 103;129;348;646, 103;254, 103;254;256;348;444;494, 103;254;646,103;254;348, 103;254;348;494, 103;256, 103;256;444, 103;256;457, 103;256;494, 103;348, 103;348;444, 103;348;494, 103;444, 103;494, 103;494;646,119;129;254;348;494, 119;129;254;457;494, 119;129;256;348;457, 119;254;348;457, 119;256;348 119;256;348;494, 119;256;444, 119;348, 119;348;494, 185;415;443;444;517;560, 185;415;443;444;517, 185;415;444;517;560;748, 185;415;444;517;748, 185;415;444;560, 185;415;560, 185;415;560;723, 185;415;723;748, 185;443;444;560, 185;444;446;517;560, 185;444;517;560, 185;444;517;560;723;748, 185;444;517;723, 185;444;560, 185;517;560;723,185;560, 185;560;723, 185;560;748, 254;457, 256;348, 256;494, 348, 348;444, 348;444;646, 348;457, 348;494, 415, 415;443;444;517;748, 415;443;444;560, 415;443;517;560;723, 415;443;517;723, 415;444;723, 415;444;517, 415;444;517;560;723;748, 415;444;517;560;748, 415;444;560;723, 415;444;517;560;723, 415;444;517;723;748 415;517;560;723;748, 415;444;560, 415;444;560;748, 415;444, 415;517, 415;517;560, 415;517;560;748, 415;560;723, 415;723;748, 415;723;748, 415;748, 443;444;517;560;723;748, 443;444;517;748, 443;444, 443;444;560, 443;444;723, 443;517, 444, 444;517;560, 444;517;748, 444;748, 444;517;560;723;748, 444;560;723, 444;560, 444;560;723, 444;517, 444;517;560, 444;517;723;748, 444;560;748, 444;723, 444;517;560, 444;560;723, 517;560, 517;560;748, 517;723, 517;748, 517;748, 560, 723, 및 723;748로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 300을 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0013] 본 발명은 또한, 서열 번호: 1262와 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 24, 24;27;28;701;729, 24;28;56;308;379;701, 24;28;56;701, 24;28;71;701, 24;28;321;701, 24;28;457;701, 24;31;56;386;701, 24;31, 24;31;56;697, 24;31;56;701, 24;31;56;264;701;750, 24;31;71;701, 24;56;154;270;697, 24;56;697;701, 24;56;701, 24;71;701, 24;225;701, 24;484;701, 24;28, 28;31, 31;56;701, 56;71;701, 56;119;146;701, 56;154;701, 56;322;697;701, 56;658;701, 56;697;701, 56;701,56;701;711, 697, 697;701, 71;74, 71;701, 129;511;701, 154;754, 177, 410;697;701, 423;701, 431, 697, 및 701로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1262를 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0014] 본 발명은 또한, 서열 번호: 1288과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 22, 31, 31;56;264;308;379;484;547;711;750, 32, 50, 57, 69;74, 71, 71;74, 71;74;129, 71;74;145, 71;74;248, 71;74;470, 71;149, 75, 141, 및 394로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1288을 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0015] 본 발명은 또한, 서열 번호: 1036과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 2, 47, 176, 253, 255, 384, 460, 467, 536, 및 623로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1036을 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0016] 본 발명은 또한, 서열 번호: 1194와 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 12;103;119;131;233;384;444;494;S646, 12;103;119;131;233;444;494;S646, 12;103;119;233;384;444;494;S646, 12;103;119;233;444;467;494;S646, 12;103;119;233;444;494;536;S646, 12;103;119;233;444;494;S646, 12;103;131;233;444;467;494;S646, 12;103;131;233;444;494;S646, 12;103;233;444;494;S646, 12;119;233;384;444;494;S646, 28;264;384;467;484;536;547, 103;119;131;233;384;444;494;S646, 103;119;233;444;494;S646, 103;233;444;494;S646, 264;384;467;484;536;547, 384;467;484;536;547, 및 668로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1194를 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0017] 본 발명은 또한, 서열 번호: 1288과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 20;709, 27, 27;74;253;254, 27;74;253;254;255;348;369;370;381, 27;74;253;254;255;348;370;384, 27;74;253;254;255;369;370, 27;74;253;254;255;370, 27;74;253;254;255;370;381;384, 27;74;253;254;255;381, 27;74;253;254;348,

27;74;253;254;384, 27;74;253;255, 27;74;253;255;348;370;384, 27;74;253;255;348;381, 27;74;253;255;348;384, 27;74;253;348;369;370, 27;74;253;348;369;370;381, 27;74;253;348;369;370;381;384, 27;74;253;348;370, 27;74;253;381;384, 27;74;253;384, 27;74;254;255;348, 27;74;254;255;348;369;370;381, 27;74;254;255;348;370, 27;74;254;255;348;381, 27;74;254;255;381, 27;74;254;348;381;384, 27;74;254;369;370, 27;74;255;348, 27;74;255;348;369;370, 27;74;255;348;369;381;384, 27;74;255;370, 27;74;348, 27;74;369;370, 27;74;107;255;348;369;370, 27;74;253, 27;74;253;254;255, 27;74;253;254;255;348;370, 27;74;253;254;348;369;370;381, 27;74;253;254;348;369;384, 27;74;253;254;348;370, 27;74;253;254;348;370;381, 27;74;253;254;369, 27;74;253;254;370;381, 27;74;253;255;348;369;370, 27;74;253;255;370, 27;74;253;348, 27;74;253;348;370;381;384, 27;74;253;369;381;384, 27;74;254,27;74;254;255;348;369;381, 27;74;254;255;348;370;381, 27;74;254;255;369, 27;74;254;348, 27;74;254;348;369;381;384, 27;74;254;348;370, 27;74;254;348;370;381, 27;74;254;384, 27;74;255;348;370, 27;74;348;384, 27;74;253;254;255;348;369;370, 27;74;253;254;348;369, 27;74;253;254;348;369;370, 27;74;253;254;348;370;381;384, 27;74;253;254;348;381;384, 27;74;253;370, 27;74;254;255;348;369;370, 27;74;254;255;348;381;384, 27;74;370, 27;74;253;254;255;348, 27;74;253;255;348;370;381, 27;74;253;255;384, 27;74;253;348;369;370;384, 27;74;253;348;381, 27;74;254;255;348;369;384, 27;74;254;255;348;370;381;384, 27;74;254;255;370, 27;74;254;348;381, 27;74;254;369;384, 27;74;255, 27;74;255;348;369;381, 27;74;348;370, 27;74;369;370;381;384, 27;253, 27;253;254, 27;253;254;255, 27;253;254;255;260;348;381;384, 27;253;254;255;348, 27;253;254;255;348;369;370;381;384, 27;253;254;255;348;369;384, 27;253;254;255;348;370, 27;253;254;255;348;370;384, 27;253;254;255;348;381;384, 27;253;254;348, 27;253;254;348;370;381, 27;253;254;348;370;384, 27;253;254;348;381, 27;253;254;348;381;384, 27;253;254;348;384, 27;253;254;381, 27;253;254;381;384, 27;253;254;384, 27;253;255;348, 27;253;255;348;369;370, 27;253;255;348;381, 27;253;255;348;384, 27;253;255;370, 27;253;255;370;381;384, 27;253;348, 27;253;348;370;381;384, 27;253;348;370;384, 27;253;348;381;384, 27;253;369;370, 27;253;381;384, 27;254;255, 27;254;255;348, 27;254;255;348;369;370, 27;254;255;348;370, 27;254;255;348;370;381, 27;254;255;348;370;381;384, 27;254;255;348;370;384, 27;254;255;369;370;381;384, 27;254;255;370, 27;254;255;381;384, 27;254;255;384, 27;254;348;369;370;381;384, 27;254;348;370, 27;254;348;381;384, 27;254;348;384, 27;254;369;381;384, 27;254;449, 27;254;470, 27;255;348, 27;255;348;370, 27;255;348;370;381;384, 27;255;348;381;384, 27;255;370, 27;348, 27;348;369;370;381;384, 27;348;381, 27;348;384, 69, 74;253;254;369;370, 74;254;255;348;384, 84, 128, 131, 132, 133, 134, 253, 253;348;370, 254, 255, 255;348;370, 256, 317;380, 348;467, 370, 373, 377, 381, 381;672, 383, 384, 388, 453, 457, 467, 472, 615, 616, 618, 619, 620, 623, 627, 701, 705, 706, 708, 및 709로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1288을 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0018] 본 발명은 또한, 서열 번호: 1262와 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하고, 하나 이상의 아미노산 위치에 적어도 하나의 치환 또는 24;31;56;701, 24;31;56;701, 24;31;71;701, 24;56;701, 및 71;74로부터 선택되는 치환 세트를 포함하는 폴리펩티드 서열을 포함하며, 상기 위치는 서열 번호: 1262를 참조로 하여 넘버링된 것인 조작된 페니실린 G 아실라제를 제공한다.

[0019] 본 발명은 서열 번호: 3-1901 중 홀수 번호의 서열에 제공된 적어도 하나의 서열과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 서열을 포함하는 조작된 페니실린 G 아실라제를 제공한다.

[0020] 본 발명은 본원에 제공된 적어도 하나의 페니실린 G 아실라제를 포함하는 조성물을 추가로 제공한다. 일부 실시양태에서, 조성물은 적어도 하나의 고정화된 페니실린 G 아실라제를 포함한다.

[0021] 본 발명은 또한 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및/또는 1287로부터 선택되는 서열과 적어도 약 85%, 약 86%, 약 87%, 약 88%, 약 89%, 약 90%, 약 91%, 약 92%, 약 93%, 약 94%, 약 95%, 약 96%, 약 97%, 약 98%, 약 99% 또는 그 이상의 서열 동일성을 가지는 폴리뉴클레오티드 서열에 의해 코딩된 페니실린 G 아실라제를 제공한다. 일부 실시양태에서, 페니실린 G 아실라제를 코딩하는 폴리뉴클레오티드 서열은 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및/또는 1287로부터 선택되는 서열과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상의 서열 동일성을 가진다. 일부 실시양태에서, 폴리뉴클레오티드 서열은 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및/또는 1287로부터 선택된다. 일부 실시양태에서, 조작된 폴리뉴클레오티드 서열은 서열 번호: 3-1901 중 홀수 번호의 서열에 제공된 적어도 하나의 서열과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 서열을 포함한다.

[0022] 본 발명은 또한 본원에 제공된 폴리뉴클레오티드 서열(예컨대, 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및/또는 1287)을 포함하는 벡터를 제공한다. 본 발명은 또한 본원에 제공된 벡터(예컨대, 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및/또는 1287의 폴리뉴클레오티드 서열을 포함하는 벡터)를 포함하는 숙주 세포를 제공한다. 일부 실시양태에서, 벡터는 서열 번호: 3-1901 중 홀수 번호의 서열에 제공된 적어도 하나의 서열과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 서열을 포함하는 적어도 하나의 조작된 폴리뉴클레오티드 서열을 포함한다.

[0023] 본 발명은 본원에 제공된 벡터를 포함하는 숙주 세포를 제공한다. 일부 실시양태에서, 숙주 세포는 원핵생물 또는 진핵생물 세포이다. 일부 추가의 실시양태에서, 숙주 세포는 박테리아 세포이다. 일부 추가의 실시양태에서, 숙주 세포는 이. 콜라이(*E. coli*)이다.

[0024] 본 발명은 본원에 제공된 적어도 하나의 조작된 페니실린 G 아실라제를 포함하는 조성물을 추가로 제공한다. 추가로, 본 발명은 조작된 페니실린 G 아실라제가 생산되는 조건하에서 본원에 제공된 숙주 세포를 배양하는 단계를 포함하는, 본원에 제공된 조작된 페니실린 G 아실라제를 제조하는 방법을 제공한다. 일부 실시양태에서, 본 방법은 제조된 조작된 페니실린 G 아실라제를 회수하는 단계를 추가로 포함한다.

[0025] 본 발명은 또한 i) 본원에 제공된 적어도 하나의 조작된 페니실린 G 아실라제 및/또는 본원에 제공된 적어도 하나의 조작된 페니실린 G 아실라제를 포함하는 조성물, 및 A1/B1/B29 트리-페닐 아세테이트 보호기를 포함하는 인슐린 또는 유리 인슐린을 제공하는 단계; 및 ii) 조작된 페니실린 G 아실라제가 A1/B1/B29 트리-페닐 아세테이트 보호기를 제거하고, 유리 인슐린, 이중 보호된 인슐린 또는 단일 보호된 인슐린이 생산되는 조건하에서 조작된 페니실린 G 아실라제를 A1/B1/B29 트리-페닐 아세테이트 보호기를 포함하는 인슐린에 노출시키는 단계; iii) 조작된 페니실린 G 아실라제가 페닐 아세테이트 보호기를 부가하고, 삼중 보호된 인슐린, 이중 보호된 인슐린 또는 단일 보호된 인슐린이 생산되는 조건하에서 조작된 페니실린 G 아실라제를 인슐린에 노출시키는 단계를 포함하는, 페닐 아세테이트 보호된 인슐린을 제조하는 방법을 제공한다. 본 발명의 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 약 85%, 약 86%, 약 87%, 약 88%, 약 89%, 약 90%, 약 91%, 약 92%, 약 93%, 약 94%, 약 95%, 약 96%, 약 97%, 약 98%, 약 99% 또는 그 이상 동일하다. 본 발명의 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하다. 본 발명의 일부 추가의 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288을 포함한다. 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4-1902에 제공된 적어도 하나의 짝수 번호의 서열과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하다. 일부 실시양태에서, 조작된 페니실린 G 아실라제는 야생형 페니실린 G 아실라제보다 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 초과 또는 그 이상으로 유리 인슐린을 생산한다. 본 발명은 또한 본 발명의 방법을 사용하여 제조된 유리 인슐린을 포함하는 조성물을 제공한다. 일부 실시양태에서, 본 발명은 본원에 제공된 임의의 방법에 따라 제조된 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 포함하는 조성물을 제공한다.

[0026] 본 발명은 또한 i) 본원에 제공된, 적어도 하나의 조작된 페니실린 G 아실라제 및/또는 적어도 하나의 조작된 페니실린 G 아실라제를 포함하는 조성물, 및 유리 인슐린을 제공하는 단계; 및 ii) 조작된 페니실린 G 아실라제가 A1, B1, 및/또는 B29 위치를 아실화시키는 조건하에서 조작된 페니실린 G 아실라제를 인슐린에 노출시킴으로써 단일 보호된 또는 이중 보호된 인슐린을 제조하는 단계를 포함하는, 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 제조하는 방법을 제공한다. 일부 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1 위치를 아실화시키는 반면, 일부 다른 실시양태에서, 페니실린 G 아실라제는 인슐린의 B1 위치를 아실화시키고 또 다른 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 B29 위치를 아실화시킨다. 일부 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1, B1, 및 B29 위치를 아실화시킨다. 일부 추가의 실시양태에서, 조작된 페니실린 G 아실라제는, 서열 번호: 2의 폴리펩티드에 의한 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린의 생산과 비교하였을 때, 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 초과 또는 그 이상으로 생산한다. 일부 추가의 실시양태에서, A1, B1 및/또는 B29를 아실화시키는 데 사용되는 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도

85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상의 동일성을 가지는 서열을 포함한다. 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4-1902에 제공된 적어도 하나의 짝수 번호의 서열과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하다.

[0027] 본 방법의 일부 추가의 실시양태에서, 페니실린 G 아실라제는 표 5.1, 6.1, 7.1, 8.1, 8.2, 9,1, 10.1, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 및/또는 12.7 중의 적어도 하나의 서열과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상의 동일성을 가지는 서열을 포함한다. 본 방법의 또 다른 추가의 실시양태에서, 페니실린 G 아실라제는 표 5.1, 6.1, 7.1, 8.1, 8.2, 9,1, 10.1, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 및/또는 12.7 중 임의의 것에 기재된 서열을 포함한다.

[0028] 본 발명은 또한 i) 제1항의 조작된 페니실린 G 아실라제, 및 인슐린을 제공하는 단계; 및 ii) 조작된 페니실린 G 아실라제가 A1, B1 및/또는 B29 트리-페닐 아세테이트 보호기를 인슐린에 부가하는 조건하에서 조작된 페니실린 G 아실라제를 인슐린에 노출시킴으로써 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 제조하는 단계를 포함하는, 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 제조하는 방법을 제공한다. 일부 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1 트리-페닐 아세테이트 보호기를 부가하는 반면, 일부 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 B1 트리-페닐 아세테이트 보호기를 부가하고, 또 다른 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 B29 트리-페닐 아세테이트 보호기를 부가한다. 일부 추가의 실시양태에서, 페니실린 G 아실라제는 인슐린의 A1, B1, 및 B29 트리-페닐 아세테이트 보호기를 부가한다. 일부 실시양태에서, 조작된 페니실린 G 아실라제는, 서열 번호: 2의 폴리펩티드에 의한 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린의 생산과 비교하였을 때, 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 초과 또는 그 이상으로 생산한다. 일부 추가의 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상의 동일성을 가지는 서열을 포함한다. 일부 실시양태에서, 페니실린 G 아실라제는 서열 번호: 4-1902에 제공된 적어도 하나의 짝수 번호의 서열과 적어도 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일하다.

[0029] 본 발명은 또한 본원에 제공된 방법 중 임의의 것에 따라 제조된 페닐 아세테이트 단일 보호된 또는 이중 보호된 인슐린을 포함하는 조성물을 제공한다.

[0030] 본 발명은, 페니실린 G 아실라제가 서열 번호: 837, 897, 1219, 또는 1859를 포함하는 방법을 추가로 제공한다.

도면의 간단한 설명

[0031] **도면의 간단한 설명**

도 1은 인슐린을 정량화하는 데 사용된 분석 방법의 크로마토그램, 및 아실화된 생성물의 용출 순서를 제공한다.

도 2a 내지 도 2h는 실시예 11에 기술된 실험 결과를 제공한다.

발명을 실시하기 위한 구체적인 내용

[0032] **본 발명의 설명**

[0033] 본 발명은 매우 다양한 β 락탐 항생제의 합성에서 중요한 중간체인, 페닐 아세트산 및 6-아미노페니실란산(6-APA)으로 페니실린을 절단할 수 있는 조작된 페니실린 G 아실라제(PGA)를 제공한다. 특히, 본 발명은 보호기를 유리 인슐린의 A1, B1 또는 B29 위치에 부가함으로써, 또는 A1/B1/B29 삼중 보호된 인슐린으로부터 보호기를 제거하거나, 또는 A1/B1/B29 트리-페닐 아세테이트 보호기를 제거함으로써 유리 인슐린을 방출할 수 있는 조작된 PGA를 제공한다.

[0034] 일반적으로, 자연적으로 발생된 PGA는 알파 서브유니트 및 베타 서브유니트로 구성된 이종이량체 효소이다. 야생형 PGA는 주변 세포질로의 이동을 매개하는 N 말단 신호 펩티드 및 알파 서브유니트의 C 말단을 베타 서브유니트의 N 말단에 연결시키는 링커 영역을 함유하는, 프리-프로-PGA 폴리펩티드로서 천연적으로 합성된다. 단백질가수분해 프로세싱은 성숙한 이종이량체 효소를 유도한다. 분자간 링커 영역은 또한 효소의 적절한 폴딩을 촉진시키는 작용을 할 수 있다. 본원에 제공된 PGA는 하기에 상세하게 기술되는 바와 같은 개선된 효소 특성을 생성하기 위해 다양한 변형이 도입된, 클루이베라 시트로필라(*Kluyvera citrophila*) 유래의 PGA를 기반으로 한다.

[0035] 본원에 제공된 설명에서, 단수의 사용은 달리 구체적으로 언급되지 않는 한, 복수의 것을 포함한다(그리고 그

반대의 경우도 그러하다). 예를 들어, 단수 형태인 "하나"("a," "an") 및 "그"는 문맥상 달리 명백하게 명시되지 않는 한, 복수의 지시 대상을 포함한다. 유사하게, "포함하다(comprise)," "포함하다(comprises)," "포함하는(comprising)," "포함하다(include)," "포함하다(includes)", 및 "포함하는(including)"은 상호교환적일 수 있고, 제한하고자 하는 것이 아니다. 다양한 실시양태의 설명에서 "포함하는"이라는 용어가 사용되는 경우, 당업자는 일부 구체적인 경우에서, 한 실시양태는 "~으로 실질적으로 구성된" 또는 "~으로 구성된"이라는 표현을 사용하여 대안적으로 기술될 수 있다는 것을 이해하게 된다는 것을 추가로 이해하여야 한다.

[0036] 도면을 비롯한, 상기의 일반 설명, 및 하기의 상세한 설명, 이 둘 모두는 오직 예시적이고, 설명적인 것이며, 본 개시내용을 제한하지 않는다. 더욱이, 본원에서 사용된 섹션 표제는 오직 조직화를 위한 것이며, 기술된 주제를 제한하는 것으로 해석되지 않아야 한다.

[0037] **정의**

[0038] 본원에서 사용되는 바, 하기 용어는 하기 의미를 가지는 것으로 의도된다.

[0039] 본 개시내용과 관련하여, 본원의 설명에서 사용되는 기술 및 과학 용어는 구체적으로 달리 정의되지 않는 한, 당업자가 보편적으로 이해하는 의미를 가질 것이다. 따라서, 하기 용어들은 하기 의미를 가지는 것으로 의도된다. 본원에 인용된, 모든 특허 및 공개문헌은, 상기 특허 및 공개문헌 내에 개시된 모든 서열을 포함하여 명백하게 참조로 포함된다. 달리 명시되지 않는 한, 본 발명의 실시는 당업자에게 알려진, 분자 생물학, 발효, 미생물학, 및 관련 분야에서 보편적으로 사용되는 통상의 기술을 포함한다. 본원에서 달리 정의되지 않는 한, 본원에서 사용되는 모든 기술 및 과학 용어는 본 발명이 속하는 분야의 숙련가가 보편적으로 이해하는 것과 동일한 의미를 가진다. 본원에 기술된 것과 유사하거나 또는 등가인 임의의 방법 및 물질이 본 발명의 실시 또는 시험에서 사용될 수 있지만, 바람직한 방법 및 물질이 기술된다. 실제로, 본 발명은 방법, 프로토콜, 및 시약이 사용되는 맥락에 따라 달라질 수 있는 바, 본원에 기술된 특정 방법, 프로토콜, 및 시약으로 제한되지 않는 것으로 의도된다. 본원에 제공된 표제는 본 발명의 다양한 측면 또는 실시양태의 제한이 아니다.

[0040] 그럼에도 불구하고, 본 발명의 이해를 촉진시키기 위해, 다수의 용어가 하기에서 정의된다. 수치 범위는 그 범위를 한정하는 수치를 포함한다. 따라서, 본원에 개시된 모든 수치 범위는, 더 좁은 수치 범위가 모두 본원에 명백하게 기재된 것처럼, 더 넓은 수치 범위에 속하는 상기 모든 좁은 수치 범위를 포함하는 것으로 의도된다. 또한, 본원에 개시된 모든 최대(또는 최소) 한계는 더 낮은(또는 더 높은) 수치 한계가 본원에 명백하게 기재된 것처럼, 상기 모든 더 낮은(또는 더 높은) 수치 한계를 포함하는 것으로 의도된다.

[0041] 본원에서 사용되는 바, "포함하는(comprising)"이라는 용어 및 그의 동족어는 그의 포괄적인 의미(즉, "포함하는(including)"이라는 용어 및 그의 동족어와 등가)로 사용된다.

[0042] 본원 및 첨부된 특허청구범위에서 사용되는 바, 단수 "하나"("a," "an") 및 "그"는 문맥상 달리 명백하게 명시되지 않는 한, 복수의 지시 대상을 포함한다. 따라서, 예를 들어, 한 "숙주 세포"에 대한 언급은 복수 개의 상기 숙주 세포를 포함한다.

[0043] 달리 명시되지 않는 한, 각각, 핵산은 좌측에서 우측으로 5'에서 3' 방향으로 및 아미노산 서열은 좌측에서 우측으로 아미노에서 카복시 방향으로 기재된다.

[0044] 본원에 제공된 표제는 전체로서 본 명세서에 참조될 수 있는 본 발명의 다양한 측면 또는 실시양태의 제한이 아니다. 따라서, 하기 정의되는 용어들은 전체로 본 명세서를 참조하여 더욱 상세하게 정의된다.

[0045] 본원에서 사용되는 바, "단백질," "폴리펩티드," 및 "펩티드"라는 용어는 본원에서 상호교환적으로 사용되고, 이는 길이 또는 번역후 변형(예컨대, 글리코실화, 인산화, 지질화, 미리스틸화, 유비퀴틴화 등)과 상관없이, 아미드 결합에 의해 공유적으로 연결된 적어도 2개의 아미노산으로 이루어진 중합체를 의미한다. D-아미노산 및 L-아미노산, 및 D-아미노산과 L-아미노산의 혼합물이 본 정의에 포함된다.

[0046] 본원에서 사용되는 바, "폴리뉴클레오티드" 및 "핵산'은 함께 공유적으로 연결된 2개 이상의 뉴클레오시드를 지칭한다. 폴리뉴클레오티드는 전체로 리보뉴클레오시드(즉, RNA)로 구성되거나, 전체로 2' 데옥시리보뉴클레오티드(즉, DNA) 또는 리보뉴클레오시드 및 2' 데옥시리보뉴클레오시드의 혼합물로 구성될 수 있다. 뉴클레오시드는 전형적으로 표준 포스포디에스테르 연결을 통해 함께 연결되지만, 폴리뉴클레오티드는 하나 이상의 비표준 연결을 포함할 수 있다. 폴리뉴클레오티드는 단일 가닥, 또는 이중 가닥일 수 있거나, 또는 단일 가닥 영역 및 이중 가닥 영역, 둘 모두를 포함할 수 있다. 더욱이, 폴리뉴클레오티드가 전형적으로 자연적으로 발생된 코딩 핵염기(즉, 아데닌, 구아닌, 우라실, 티민, 및 시토신)로 구성되는 반면, 하나 이상의 변형된 핵염기 및/또는 합성 핵

염기(예컨대, 이노신, 크산틴, 히포크산틴 등)를 포함할 수 있다. 바람직하게, 상기 변형된 핵염기 또는 합성 핵염기는 코딩 핵염기가 될 것이다.

[0047] 본원에서 사용되는 바, "하이브리드화 엄격성"은 핵산의 하이브리드화시, 세척 조건과 같은, 하이브리드화 조건에 관한 것이다. 일반적으로, 하이브리드화 반응은 더 낮은 엄격성 조건하에서 수행된 후, 다양하지만, 더 높은 엄격성의 세척이 진행된다. "중간 정도로 엄격한 하이브리드화"라는 용어는 표적 DNA가, 표적 DNA와 약 60%의 동일성, 바람직하게, 약 75%의 동일성, 약 85%의 동일성을 가지는; 표적 폴리뉴클레오티드와 약 90% 초과의 동일성을 가지는 상보적인 핵산에 결합할 수 있도록 허용하는 조건을 지칭한다. 예시적인 중간 정도로 엄격한 조건은 42℃에서 50% 포름아미드, 5X 덴하르트 용액(Denhart's solution), 5XSSPE, 0.2% SDS에서 하이브리드화 후, 42℃에서 0.2XSSPE, 0.2% SDS에서 세척하는 것과 등가인 조건이다. "고엄격성 하이브리드화"는 일반적으로 정의진 폴리뉴클레오티드 서열에 대한 용해 조건하에서 측정된 바와 같은 열적 용융 온도 T_m으로부터 약 10℃ 이하인 조건을 의미한다. 일부 실시양태에서, 고엄격성 조건은 65℃에서 0.018M NaCl 중에서 안정한 하이브리드를 형성하는 오직 그들 핵산 서열만의 하이브리드화를 가능하게 하는 조건을 지칭한다(즉, 만약 하이브리드가 65℃에서 0.018M NaCl에서 안정적이지 않다면, 본원에서 고려하는 바와 같이, 고엄격성 조건하에서 안정하지 않을 것이다). 고엄격성 조건은 예를 들어, 42℃에서 50% 포름아미드, 5X 덴하르트 용액, 5XSSPE, 0.2% SDS와 등가인 조건에서 하이브리드화한 후, 이어서, 65℃에서 0.1XSSPE, 및 0.1% SDS에서 세척하는 것으로 제공될 수 있다. 또 다른 고엄격성 조건은 65℃에서 0.1%(w:v) SDS를 함유하는 5X SSC에서 하이브리드화하고, 65℃에서 0.1% SDS를 함유하는 0.1x SSC에서 세척하는 것과 등가인 조건에서 하이브리드화하는 것이다. 다른 고엄격성 하이브리드화 조건 뿐만 아니라, 중간 정도로 엄격한 조건도 당업자에게 공지되어 있다.

[0048] 본원에서 사용되는 바, "코딩 서열"은 단백질의 아미노산 서열을 코딩하는 핵산(예컨대, 유전자)의 일부를 지칭한다.

[0049] 본원에서 사용되는 바, "코돈 최적화"는 코딩된 단백질이 관심 유기체에서 효율적으로 발현되도록 하기 위한, 단백질을 코딩하는 폴리뉴클레오티드의 코돈을 특정 유기체에서 우선적으로 사용되는 것으로 변화시키는 것을 지칭한다. 일부 실시양태에서, PGA 효소를 코딩하는 폴리뉴클레오티드는 발현을 위해 선택된 숙주 유기체로부터 최적 생산을 위해 코돈 최적화될 수 있다. 비록 유전자 코돈은 대부분의 아미노산이 "동의성" 또는 "동의" 코돈이라고 불리는, 몇몇 코돈으로 대표되는 축퇴성이기는 하지만, 특정 유기체에 의한 코돈 용법은 특정 코돈 트리플렛 쪽으로의 비무작위적이고, 편향적인 것으로 널리 공지되어 있다. 이러한 코돈 용법 편향성은 주어진 유전자, 공통 기능 또는 조상 기원의 유전자들, 저카피수 단백질 대비 고발현 단백질, 및 유기체 게놈의 집합 단백질 코딩 영역과 관련하여 더 높을 수 있다. 일부 실시양태에서, PGA 효소를 코딩하는 폴리뉴클레오티드는 발현을 위해 선택된 숙주 유기체로부터 최적 생성을 위해 코돈 최적화될 수 있다.

[0050] 본원에서 사용되는 바, "바람직한, 최적의, 높은 코돈 용법 편향 코돈"은 상호교환적으로 동일한 아미노산을 코딩하는 다른 코돈보다 단백질 코딩 영역에서 더 높은 빈도로 사용되는 코돈을 지칭한다. 바람직한 코돈은 단일 유전자의 코돈 용법, 공통 기능 또는 기원의 유전자 세트, 고도로 발현되는 유전자, 전체 유기체의 집합 단백질 코딩 영역의 코돈 빈도, 관련 유기체의 집합 단백질 코딩 영역의 코돈 빈도, 또는 그의 조합과 관련하여 결정될 수 있다. 그 빈도가 유전자 발현 수주에 따라 증가하는 코돈이 전형적으로 발현에 최적인 코돈이다. 예를 들어, 군집 분석 또는 대응 분석을 사용하는, 다변량 분석, 및 유전자에서 사용되는 코돈의 유효수를 비롯한, 특정 유기체에서 코돈 빈도(예컨대, 코돈 용법, 상대적 동의 코돈 용법) 및 코돈 선호도를 결정하는 다양한 방법이 공지되어 있다(예컨대, 문헌 [GCG CodonPreference, Genetics Computer Group Wisconsin Package; CodonW, John Peden, University of Nottingham; McInerney, Bioinform., 14:372-73 [1998]]; [Stenico et al., Nucleic Acids Res., 222:437-46 [1994]; 및 [Wright, Gene 87:23-29 [1990]] 참조). 유기체 목록 증가를 위해 코돈 용법 표가 이용가능하다(예컨대, 문헌 [Wada et al., Nucleic Acids Res., 20:2111-2118 [1992]]; [Nakamura et al., Nucl. Acids Res., 28:292 [2000]]; [Duret, et al., 상기 문헌 동일]; [Henaut and Danchin, "*Escherichia coli* and *Salmonella*," Neidhardt, et al. (eds.), ASM Press, Washington D.C., [1996], p. 2047-2066] 참조). 코돈 용법을 획득하기 위한 데이터 공급원은 단백질을 코딩할 수 있는 임의의 이용가능한 뉴클레오티드 서열에 의존할 수 있다. 이들 데이터 세트는 발현되는 단백질을 코딩하는 것으로 실제로 알려진 핵산 서열(예컨대, 완전한 단백질 코딩 서열-CDS(complete protein coding sequence)), 발현된 서열 태그(ESTS: expressed sequence tags), 또는 게놈 서열의 예상되는 코딩 영역을 포함한다(예컨대, 문헌 [Uberbacher, Meth. Enzymol., 266:259-281 [1996]]; [Tiwari et al., Comput. Appl. Biosci., 13:263-270 [1997]] 참조).

[0051] 본원에서 사용되는 바, "제어 서열"은 본원에서 본 발명의 폴리뉴클레오티드 및/또는 폴리펩티드의 발현에 필요

하거나, 또는 이로운, 모든 성분을 포함하는 것으로 정의된다. 각각의 제어 서열은 관심 폴리뉴클레오티드에 천연적이거나, 또는 외래의 것일 수 있다. 그러한 제어 서열로는 리더, 폴리아데닐화 서열, 프로펩티드 서열, 프로모터, 신호 펩티드 서열, 및 전사 종결인자를 포함하나, 이에 제한되지 않는다.

[0052] 본원에서 사용되는 바, "작동가능하게 연결된"은 본원에서 제어 서열이 관심 폴리뉴클레오티드 및/또는 폴리펩티드의 발현을 지시하거나, 또는 조절할 수 있도록 제어 서열이 관심 폴리뉴클레오티드에 대한 위치에 적절하게 배치(기능적 관계로)되어 있는 배열로서 정의된다.

[0053] 본원에서 사용되는 바, "프로모터 서열"은 예컨대, 코딩 서열과 같은, 관심 폴리뉴클레오티드의 발현을 위해 숙주 세포에 의해 인식되는 핵산 서열을 지칭한다. 제어 서열은 적절한 프로모터 서열을 포함할 수 있다. 프로모터 서열은 관심 폴리뉴클레오티드의 발현을 매개하는 전사 제어 서열을 함유한다. 프로모터는 돌연변이체, 말단 절단형, 및 하이브리드 프로모터를 비롯한, 선택된 숙주 세포 내에서 전사 활성을 보이는 임의의 핵산 서열일 수 있고, 숙주 세포에 상동성이거나 또는 이종성인 세포외 또는 세포내 폴리펩티드를 코딩하는 유전자로부터 수득될 수 있다.

[0054] 본원에서 사용되는 바, "자연적으로 발생된" 또는 "야생형"은 자연상에서 발견되는 형태를 지칭한다. 예를 들어, 자연적으로 발생된 또는 야생형 폴리펩티드 또는 폴리뉴클레오티드 서열은 자연상의 공급원으로부터 단리될 수 있고, 인간 조작에 의해 의도적으로 변형되지 않은 유기체에 존재하는 서열이다.

[0055] 본원에서 사용되는 바, (예컨대, 세포, 핵산, 또는 폴리펩티드)와 관련하여, 본 개시내용에서 사용될 때, "비자연적으로 발생된," "조작된," 및 "재조합"은 달리 자연상에 존재하지 않는 방식으로 변형된, 물질, 또는 상기 물질의 자연 또는 천연 형태에 상응하는 물질을 지칭한다. 일부 실시양태에서, 물질은 자연적으로 발생된 물질과 동일하지만, 합성 물질로부터 및/또는 재조합 기술을 사용하는 조작에 의해 제조 또는 유도된 것이다. 비제한적인 예로는 다른 것들 중에서도 특히 세포의 천연(비재조합) 형태에서는 발견되지 않거나, 또는 그렇지 않으면 다른 수준으로 발현되는 천연 유전자를 발현하는 유전자를 발현하는 재조합 세포를 포함한다.

[0056] 본원에서 사용되는 바, "서열 동일성(%)" "동일성(%)" 및 "% 동일"은 폴리뉴클레오티드 서열 사이 및 폴리펩티드 서열 사이의 비교를 지칭하고, 비교창에 걸쳐 최적으로 정렬된 두 서열을 비교함으로써 측정되고, 여기서, 상기 비교창의 폴리뉴클레오티드 또는 폴리펩티드 서열의 일부분은 두 서열의 최적의 정렬을 위해, 참조 서열과 비교하여 부가 또는 결실(즉, 갭)을 포함할 수 있다. 백분율(%)은 동일한 핵산 염기 또는 아미노산 잔기가 두 서열 모두에 존재하는 위치, 또는 핵산 염기 또는 아미노산 잔기가 갭과 함께 정렬된 위치의 개수를 측정하여 매칭되는 위치의 개수를 산출하고, 매칭되는 위치의 개수를 비교창 중 위치의 총 개수로 나누고, 그 결과에 100을 곱하여 서열 동일성(%)을 산출함으로써 계산된다. 최적의 정렬 및 서열 동일성(%) 측정은 BLAST 및 BLAST 20 알고리즘을 사용하여 수행된다(예컨대, 문헌 [Altschul et al., J. Mol. Biol. 215: 403-410 [1990]]; 및 [Altschul et al., Nucl. Acids Res. 3389-3402 [1977]] 참조). BLAST 분석을 수행하기 위한 소프트웨어는 미국 국립 생명공학 정보 센터(National Center for Biotechnology Information)의 웹사이트를 통해 공개적으로 이용가능하다.

[0057] 간략하면, BLAST 분석은 먼저, 데이터베이스 서열 중에서 길이가 동일한 워드와 정렬되었을 때, 일부 양성 값 역치 점수(T)와 매칭되거나, 또는 그를 만족하는 질의 서열 중의 짧은 워드 길이(W)를 확인함으로써 높은 점수의 서열 쌍(HSP: high scoring sequence pair)을 확인하는 것을 포함한다. T는 이웃 워드 점수 역치로서 지칭된다(문헌 [Altschul et al, 상기 문헌 동일]. 이들 초기 이웃 워드 히트는 그들을 함유하는 더 긴 HSP를 찾도록 검색을 개시하기 위한 씨드로서 작용한다. 이어서, 히트를 누적 정렬 점수가 증가될 수 있는 만큼 멀리 각 서열을 따라 양쪽 방향으로 연장시킨다. 누적 점수는 뉴클레오티드 서열의 경우, 파라미터 M(매칭되는 잔기 쌍에 대한 보상 점수; 항상 > 0임) 및 N(미스매칭되는 잔기에 대한 패널티 점수; 항상 < 0임)을 사용하여 계산된다. 아미노산 서열의 경우, 점수화 매트릭스가 누적 점수를 계산하는 데 사용된다. 각 방향으로 워드 히트의 연장은 누적 정렬 점수가 그의 최대 획득 값으로부터 정량 X만큼 하락하였을 때; 누적 점수가 하나 이상의 음수 잔기 정렬의 축적으로 인해 0 이하가 되거나; 또는 양쪽 서열의 끝에 도달하였을 때 중지된다. BLAST 알고리즘 파라미터 W, T, 및 X는 정렬의 감도 및 속도를 결정한다. BLASTN 프로그램(뉴클레오티드 서열인 경우)은 디폴트로서 워드길이(W) = 11, 기대치(E) = 10, M=5, N=-4, 및 양쪽 가닥의 비교를 사용한다. 아미노산 서열인 경우, BLASTP 프로그램은 디폴트로서 워드길이(W) = 3, 기대치(E) = 10, 및 BLOSUM62 점수화 매트릭스를 사용한다(예컨대, 문헌 [Henikoff and Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 [1989]] 참조).

[0058] 2개 서열에 대한 동일성(%)을 제공하는 데 BLAST와 유사하게 작용하는 다수의 다른 알고리즘이 당업계에서 이용가능하며, 공지되어 있다. 비교를 위한 서열의 최적의 정렬은 당업계에 공지된 임의의 적합한 방법을 사용하여

(예컨데, 문헌 [Smith and Waterman, Adv. Appl. Math. 2:482 [1981]]의 국소 상동성 알고리즘에 의해; [Needleman and Wunsch, J. Mol. Biol. 48:443 [1970]]의 상동성 정렬 알고리즘에 의해; [Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:2444 [1988]]의 유사성 검색 방법에 의해; 및/또는 상기 알고리즘([GCG 위스콘신 소프트웨어 패키지의 GAP, BESTFIT, FASTA, 및 TFASTA]의 컴퓨터 실행에 의해), 또는 당업계에 일반적으로 알려져 있는 방법을 사용하여 시각적 검사에 의해 수행될 수 있다. 추가적으로, 서열 정렬 및 서열 동일성(%) 측정은 제공된 디폴트 파라미터를 사용하여 GCG 위스콘신 소프트웨어 패키지의 BESTFIT 또는 GAP 프로그램(Accelrys, 미국 위스콘신주 매디슨 소재)을 사용할 수 있다.

[0059] 본원에서 사용되는 바, "실질적 동일성"은 적어도 20개의 잔기 위치로 이루어진 비교창, 빈번하게는 적어도 30-50개의 잔기로 이루어진 창에 걸쳐 참조 서열과 비교하였을 때, 적어도 80%의 서열 동일성, 적어도 85%의 서열 동일성 및 89 내지 95%의 서열 동일성, 더욱 일반적으로는 적어도 99%의 서열 동일성을 가지는 폴리뉴클레오티드 또는 폴리펩티드 서열을 지칭하고, 서열 동일성(%)은 비교창에 걸쳐 참조 서열의 총 20% 이하인 결실 또는 부가를 포함하는 서열과 참조 서열을 비교함으로써 계산된다. 폴리펩티드에 적용되는 구체적인 실시양태에서, "실질적 동일성"이란, 두 폴리펩티드가 최적으로 정렬되었을 때, 예컨대, 디폴트 갭 가중치를 사용하는 프로그램 GAP 또는 BESTFIT에 의해 적어도 80%의 서열 동일성, 바람직하게, 적어도 89%의 서열 동일성, 적어도 95%의 서열 동일성 또는 그 이상(예컨대, 99%의 서열 동일성)을 공유하는 것을 지칭한다. 일부 바람직한 실시양태에서, 동일하지 않은 잔기 위치는 보존적 아미노산 치환이 다르다.

[0060] 본원에서 사용되는 바, "참조 서열"은 또 다른 서열의 비교 대상이 되는 정의된 서열을 지칭한다. 참조 서열은 더 큰 서열의 서브세트, 예를 들어, 전장의 유전자 또는 폴리펩티드 서열의 세그먼트일 수 있다. 일반적으로, 참조 서열은 길이가 적어도 20개의 뉴클레오티드 또는 아미노산 잔기 길이, 적어도 25개의 잔기 길이, 적어도 50개의 잔기 길이, 또는 핵산 또는 폴리펩티드의 전장인 길이이다. 두 폴리뉴클레오티드 또는 폴리펩티드가 각각 (1) 두 서열 간에 유사한 서열(즉, 완전한 서열의 일부)을 포함하고, (2) 두 서열 간에 다른 서열을 추가로 포함할 수 있으므로, 2개(또는 그 이상의) 폴리뉴클레오티드 또는 폴리펩티드 간의 서열 비교는 전형적으로 비교창에 걸쳐 두 폴리뉴클레오티드의 서열을 비교함으로써 서열 유사성의 국소 영역을 확인하고, 비교함으로써 수행된다. "참조 서열"이라는 용어는 야생형 서열로 제한되는 것으로 의도되지 않고, 조작되거나, 또는 변경된 서열을 포함할 수 있다. 예를 들어, 일부 실시양태에서, "참조 서열"은 사전에 조작되거나, 또는 변경된 아미노산 서열일 수 있다.

[0061] 본원에서 사용되는 바, "비교창"은 적어도 약 20개의 인접한 뉴클레오티드 위치 또는 아미노산 잔기의 개념적 절편을 지칭하고, 여기서, 서열은 적어도 20개의 인접한 뉴클레오티드 또는 아미노산의 참조 서열과 비교될 수 있고, 비교창 내 서열의 일부분은 두 서열의 최적의 정렬을 위해 (부가 또는 결실을 포함하지 않는) 참조 서열과 비교하였을 때, 20% 이하의 부가 또는 결실(즉, 갭)을 포함할 수 있다. 비교창은 20개보다 긴 인접한 잔기일 수 있고, 임의적으로, 30, 40, 50, 100개, 또는 그보다 긴 창을 포함한다.

[0062] 본원에서 사용되는 바, 주어진 아미노산 또는 폴리뉴클레오티드 서열의 넘버링과 관련하여 사용할 때, "~에 상응하는," "~와 관련하여," 및 "~ 대비"는 주어진 아미노산 또는 폴리뉴클레오티드 서열을 참조 서열과 비교하는 경우의 언급된 참조 서열의 잔기의 넘버링을 지칭한다. 다시 말해, 주어진 중합체의 잔기 번호 또는 잔기 위치는 주어진 아미노산 또는 폴리뉴클레오티드 서열 내 잔기의 실제 번호 위치보다는 참조 서열에 대해 지정된다. 예를 들어, 주어진 아미노산 서열, 예컨대, 조작된 PGA의 아미노산 서열은 두 서열 사이의 잔기 매치를 최적화하기 위해 갭을 도입시킴으로써 참조 서열에 대해 정렬시킬 수 있다. 이러한 경우, 비록 갭이 존재하여도, 주어진 아미노산 또는 폴리뉴클레오티드 서열 내 잔기의 넘버링은 정렬시킨 참조 서열에 대해 이루어진다. 본원에서 사용되는 바, 하기에서 추가로 기술되는 바와 같이, 잔기 위치, 예컨대, "Xn"에 대한 언급은 달리 구체적으로 언급되지 않는 한, "~에 상응하는 잔기"를 지칭하는 것으로 이해되어야 한다. 따라서, 예를 들어, "X94"는 폴리펩티드 서열에서 94번 위치의 임의의 아미노산을 지칭한다.

[0063] 본원에서 사용되는 바, "개선된 효소 특성"은 참조 PGA와 비교하였을 때, 임의의 효소 특성의 개선을 나타내는 PGA를 지칭한다. 비록 일부 실시양태에서, 참조 PGA는 또 다른 개선된 조작된 PGA일 수 있지만, 본원에 기술된 조작된 PGA 폴리펩티드의 경우, 비교는 일반적으로 야생형 PGA 효소에 대해 이루어진다. 개선이 바람직할 수 있는 효소 특성으로는 효소 활성(명시된 양의 PGA를 사용한 명시된 반응 시간에서의 기질의 전환율(%)로 표시될 수 있다), 화학선택성, 열 안정성, 용매 안정성, pH 활성 프로파일, 보조인자 요구, 억제제에 대한 무반응성(예컨대, 생성물 억제), 입체특이성 및 입체선택성(거울상 선택성 포함)을 포함하나, 이에 제한되지 않는다.

[0064] 본원에서 사용되는 바, "증가된 효소 활성"은 참조 PGA 효소와 비교하여 비활성(예컨대, 제조된 생성물/시간/단

백질 중량)의 증가 또는 기질의 생성물로의 전환율(%)(예컨대, 명시된 양의 PGA를 사용한 명시된 기간 동안 출발량의 기질의 생성물로의 전환율(%))의 증가로 표현될 수 있는, 조작된 PGA 폴리펩티드의 개선된 특성을 지칭한다. 효소 활성을 측정하는 예시적인 방법은 실시예에 제공되어 있다. 그의 변화가 효소 활성을 증가시킬 수 있는 것인 K_m, $V_{최대}$ 또는 k_{cat}인 고전적인 효소 특성을 비롯한, 효소 활성과 관련된 임의의 특성이 영향을 받을 수 있다. 효소 활성의 개선은 상응하는 야생형 PGA 효소의 효소 활성의 약 1.5배부터, 자연적으로 발생된 PGA, 또는 PGA 폴리펩티드 유래 기점이 된 또 다른 조작된 PGA보다 2배, 5배, 10배, 20배, 25배, 50배, 75배, 100배 이상만큼의 효소 활성일 수 있다. 구체적인 실시양태에서, 조작된 PGA 효소는 모체 PGA 효소보다 1.5 내지 50배, 1.5 내지 100배 범위로 더 큰 개선된 효소 활성을 나타낸다. 임의의 효소의 활성은 확산 제한적인 바, 이에 촉매 전환 속도는 임의의 필요한 보조인자를 비롯한, 기질의 확산 속도를 초과할 수 없다는 것을 당업자는 이해한다. 확산 한계, 또는 k_{cat}/K_m의 이론상 최대값은 일반적으로 약 10^8 내지 10^9 (M^{-1} s^{-1})이다. 따라서, PGA의 효소 활성의 임의의 개선은 PGA 효소에 의해 작용을 받는 기질의 확산 속도와 관련된 상한계를 가지게 된다. PGA 활성은 페니실린 G의 절단시 페닐아세트산의 방출을 측정하기 위해 사용되는 표준 검정법 중 어느 하나, 예컨대, 적정법에 의해 측정될 수 있다(예컨대, 문헌 [Simons and Gibson, Biotechnol. Tech.,13:365-367 [1999]] 참조) . 일부 실시양태에서, PGA 활성은 절단 생성물 5-아미노-2-니트로-벤조산을 분광광도법으로 검출 가능한(λ최대 = 405 nm), 6-니트로페닐아세트아미도 벤조산(NIPAB)을 사용하여 측정될 수 있다. 효소 활성의 비교는 본원에 상세하게 추가로 기술되는 바와 같이, 정의된 효소 제제, 설정된 조건하에서의 정의된 검정법, 및 하나 이상의 정의된 기질을 사용하여 이루어진다. 일반적으로, 용해물을 비교하는 경우, 숙주 세포에 의해 생산되고, 용해물에 존재하는 효소의 양의 변동을 최소화하기 위해 동일한 발현 시스템 및 동일한 숙주 세포를 사용하는 것 뿐만 아니라, 세포의 개수 및 검정되는 단백질의 양을 측정한다.

[0065] 본원에서 사용되는 바, "증가된 효소 활성" 및 "증가된 활성"은 본원에 기술된 바와 같이 참조 효소와 비교하여 비활성(예컨대, 제조된 생성물/시간/단백질 중량)의 증가 또는 기질의 생성물로의 전환율(%)(예컨대, 명시된 양의 PGA를 사용한 명시된 기간 동안 출발량의 기질의 생성물로의 전환율(%))의 증가로 표현될 수 있는, 조작된 효소의 개선된 특성을 지칭한다. 그의 변화가 효소 활성을 증가시킬 수 있는 것인 K_m, $V_{최대}$ 또는 k_{cat}인 고전적인 효소 특성을 비롯한, 효소 활성과 관련된 임의의 특성이 영향을 받을 수 있다. 일부 실시양태에서, 본원에 제공된 PGA 효소는 인슐린의 특정 잔기로부터 트리-페닐 아세테이트 보호기를 제거하여 인슐린을 유리시킨다. 효소 활성의 비교는 본원에 상세하게 추가로 기술되는 바와 같이, 정의된 효소 제제, 설정된 조건하에서의 정의된 검정법, 및 하나 이상의 정의된 기질을 사용하여 이루어진다. 일반적으로, 세포 용해물 중의 효소를 비교하는 경우, 숙주 세포에 의해 생산되고, 용해물에 존재하는 효소의 양의 변동을 최소화하기 위해 동일한 발현 시스템 및 동일한 숙주 세포를 사용하는 것 뿐만 아니라, 세포의 개수 및 검정되는 단백질의 양을 측정한다.

[0066] 본원에서 사용되는 바, 본원에서 사용되는 바, "전환"은 기질의 상응하는 생성물로의 효소적 변환을 지칭한다.

[0067] 본원에서 사용되는 바, "전환율"은 특정 조건하에서 일정 기간 이내에 생성물로 전환되는 기질의 비율을 지칭한다. 따라서, 예를 들어, PGA 폴리펩티드의 "효소 활성" 또는 "활성"은 기질의 생성물로의 "전환율(%)"로서 표현될 수 있다.

[0068] 본원에서 사용되는 바, "화학선택성"은 화학 또는 효소 반응에서 다른 것보다 한 생성물의 우선적 형성을 지칭한다.

[0069] 본원에서 사용되는 바, "열안정성" 및 "열적 안정한"은 상호교환적으로 사용되고, 이는 미처리 효소와 비교하여 일정 기간(예컨대, 0.5-24 hr) 동안 온도 조건 세트(예컨대, 40-80℃)에 노출되었을 때, 불활성화에 대하여 내성을 띠고, 이로써, 상승된 온도에의 노출 후에도 일정 수준의 잔류 활성(예컨대, 60% 내지 80% 초과)을 유지하는 폴리펩티드를 지칭한다.

[0070] 본원에서 사용되는 바, "용매 안정성"은 미처리 효소와 비교하여 일정 기간(예컨대, 0.5-24 hr) 동안 다양한 농도(예컨대, 5-99%)의 용매(예컨대, 이소프로필 알콜, 테트라히드로퓨란, 2-메틸테트라히드로퓨란, 아세톤, 톨루엔, 부틸아세테이트, 메틸 tert-부틸에테르 등)에의 노출 후에도 유사한 활성(예컨대, 60% 내지 80% 초과)을 유지할 수 있는 폴리펩티드의 능력을 지칭한다.

[0071] 본원에서 사용되는 바, "pH 안정성"은 미처리 효소와 비교하여 일정 기간(예컨대, 0.5-24 hr) 동안 높거나 또는 낮은 pH(예컨대, 4.5-6 또는 8 내지 12)에의 노출 후도 유사한 활성(예컨대, 60% 내지 80% 초과)을 유지하는 PGA 폴리펩티드를 지칭한다.

[0072] 본원에서 사용되는 바, "열 및 용매 안정성"은 열안정성이자, 용매 안정성인 PGA 폴리펩티드를 지칭한다.

[0073] 본원에서 사용되는 바, "친수성 아미노산 또는 잔기"는 (Eisenberg et al.)(문헌 [Eisenberg et al., J. Mol. Biol., 179:125-142 [1984]])의 정규화된 공통 소수성 척도에 따라 0 미만인 소수성을 나타내는 측쇄를 가지는 아미노산 또는 잔기를 지칭한다. 유전적으로 코딩되는 친수성 아미노산으로는 L-Thr(T), L-Ser(S), L-His(H), L-Glu(E), L-Asn(N), L-Gln(Q), L-Asp(D), L-Lys(K) 및 L-Arg(R)를 포함한다.

[0074] 본원에서 사용되는 바, "산성 아미노산 또는 잔기"는 아미노산이 펩티드 또는 폴리펩티드에 포함될 때 약 6 미만인 pK 값을 나타내는 측쇄를 가지는 친수성 아미노산 또는 잔기를 지칭한다. 산성 아미노산은 전형적으로 수소 이온의 손실로 인해 생리학적 pH에서 음으로 하전된 측쇄를 가진다. 유전적으로 코딩되는 산성 아미노산으로는 L-Glu(E) 및 L-Asp(D)를 포함한다.

[0075] 본원에서 사용되는 바, "염기성 아미노산 또는 잔기"는 아미노산이 펩티드 또는 폴리펩티드에 포함될 때 약 6 초과인 pK 값을 나타내는 측쇄를 가지는 친수성 아미노산 또는 잔기를 지칭한다. 염기성 아미노산은 전형적으로 히드로늄 이온과의 회합에 기인하여 생리적 pH에서 양으로 하전된 측쇄를 가진다. 유전적으로 코딩되는 염기성 아미노산으로는 L-Arg(R) 및 L-Lys(K)을 포함한다.

[0076] 본원에서 사용되는 바, "극성 아미노산 또는 잔기"는 생리적 pH에서 하전되지 않지만, 2개 원자가 공통으로 공유하는 전자쌍이 원자 중 하나에 의해 더 가깝게 유지되는 적어도 하나의 결합이 있는 측쇄를 가지는 친수성 아미노산 또는 잔기를 지칭한다. 유전적으로 코딩되는 극성 아미노산으로는 L-Asn(N), L-Gln(Q), L-Ser(S) 및 L-Thr(T)을 포함한다.

[0077] 본원에서 사용되는 바, "소수성 아미노산 또는 잔기"는 (Eisenberg et al.)(문헌 [Eisenberg et al., J. Mol. Biol., 179:125-142 [1984]])의 정규화된 공통 소수성 척도에 따라 0 초과인 소수성을 나타내는 측쇄를 가지는 아미노산 또는 잔기를 지칭한다. 유전적으로 코딩되는 소수성 아미노산으로는 L-Pro(P), L-Ile I), L-Phe(F), L-Val(V), L-Leu(L), L-Trp(W), L-Met(M), L-Ala(A) 및 L-Tyr(Y)을 포함한다.

[0078] 본원에서 사용되는 바, "방향족 아미노산 또는 잔기"는 적어도 하나의 방향족 또는 헤테로방향족 고리를 포함하는 측쇄를 가지는 친수성 또는 소수성 아미노산 또는 잔기를 지칭한다. 유전적으로 코딩되는 방향족 아미노산으로는 L-Phe(F), L-Tyr(Y) 및 L-Trp(W)를 포함한다. L-His(H)는 그의 헤테로방향족 질소 원자의 pKa에 기인하여 종종 염기성 잔기로 분류되거나, 또는 그의 측쇄가 헤테로방향족 고리를 포함함에 따라, 방향족 잔기로 분류되지만, 히스티딘은 본원에서 친수성 잔기 또는 "구속형 잔기"(이하 참조)로서 분류된다.

[0079] 본원에서 사용되는 바, "구속형 아미노산 또는 잔기"는 구속형 기하학적 구조를 가지는 아미노산 또는 잔기를 지칭한다. 본원에서, 구속형 잔기로는 L-Pro(P) 및 L-His(H)를 포함한다. 히스티딘은 상대적으로 작은 이미다졸 고리를 갖고 있기 때문에, 구속형 기하학적 구조를 가진다. 프롤린 또한 5원 고리를 갖고 있기 때문에, 구속형 기하학적 구조를 가진다.

[0080] 본원에서 사용되는 바, "비극성 아미노산 또는 잔기"는 2개 원자가 공통으로 공유하는 전자쌍이 일반적으로 각각의 두 원자에 의해 동일하게 유지되는 결합을 가지며, 생리적 pH에서 비하전된 측쇄(즉, 측쇄는 극성이 아니다)를 가지는 소수성 아미노산 또는 잔기를 지칭한다. 유전적으로 코딩된 비극성 아미노산으로는 L-Gly(G), L-Leu(L), L-Val(V), L-Ile(I), L-Met(M) 및 L-Ala(A)를 포함한다.

[0081] 본원에서 사용되는 바, "지방족 아미노산 또는 잔기"는 지방족 탄화수소 측쇄를 가지는 소수성 아미노산 또는 잔기를 의미한다. 유전적으로 코딩되는 지방족 아미노산으로는 L-Ala(A), L-Val(V), L-Leu(L) 및 L-Ile(I)을 포함한다.

[0082] 시스테인(또는 "L-Cys" 또는 "[C]")은 다른 L-Cys(C) 아미노산 또는 다른 술파닐 함유 또는 술프히드릴 함유 아미노산과 이황화 브릿지를 형성할 수 있다는 점에서 일반적인 것은 아님에 주의한다. "시스테인 유사 잔기"는 이황화 브릿지를 형성하는 데 이용가능한 술프히드릴 모이어티를 함유하는 다른 아미노산과 시스테인을 포함한다. 환원된 유리-SH 또는 산화된 이황화 브릿지 형태로 펩티드에 존재할 수 있는 L-Cys(C)(및 -SH 함유 측쇄를 가지는 다른 아미노산)의 능력은 L-Cys(C)가 펩티드에 대한 순 소수성 또는 친수성 특징에 기여하는지 여부에 영향을 준다. L-Cys(C)는 (Eisenberg)(문헌 [Eisenberg et al., 1984, 상기 문헌 동일])의 정규화된 공통 스케일에 따라 0.29인 소수성을 나타내지만, 본 개시내용의 목적을 위해, L-Cys(C)는 그 자체의 고유한 군으로 분류된다는 것을 이해하여야 한다.

[0083] 본원에서 사용되는 바, "소형 아미노산 또는 잔기"는 총 3개 이하의 탄소 및/또는 헤테로원자(α-탄소 및 수소

배제)로 구성된 측쇄를 가지는 아미노산 또는 잔기를 지칭한다. 소형 아미노산 또는 잔기는 상기 정의에 따라 지방족, 비극성, 극성 또는 산성 소형 아미노산 또는 잔기로서 추가로 분류될 수 있다. 유전적으로 코딩되는 소형 아미노산으로는 L-Ala(A), L-Val(V), L-Cys(C), L-Asn(N), L-Ser(S), L-Thr(T) 및 L-Asp(D)를 포함한다.

[0084] 본원에서 사용되는 바, "히드록실 함유 아미노산 또는 잔기"는 히드록실(-OH) 모이어티를 함유하는 아미노산을 의미한다. 유전적으로 코딩되는 히드록실 함유 아미노산으로 L-Ser(S), L-Thr(T) 및 L-Tyr(Y)을 포함한다.

[0085] 본원에서 사용되는 바, "아미노산 차이" 및 "잔기 차이"는 참조 서열 중의 상응하는 위치에 있는 아미노산 잔기 대비 폴리펩티드 서열의 위치에 있는 아미노산 잔기의 차이를 지칭한다. 아미노산 차이의 위치는 일반적으로 본원에서 "Xn"으로 지칭되며, 여기서 n은 잔기 차이의 기초가 되는 참조 서열 중의 상응하는 위치를 지칭한다. 예를 들어, "서열 번호: 2와 비교하여 위치 X40에서의 잔기 차이"는 서열 번호: 2의 40번 위치에 상응하는 폴리펩티드 위치에 있는 아미노산 잔기의 차이를 지칭한다. 따라서, 서열 번호: 2의 참조 폴리펩티드가 40번 위치에 히스티딘을 가지면, 이때 "서열 번호: 2와 비교하여 위치 X40에서의 잔기 차이"란, 서열 번호: 2의 40번 위치에 상응하는 폴리펩티드의 위치에 히스티딘 이외의 다른 임의의 잔기의 아미노산 치환을 지칭한다. 본원의 대부분의 경우에서, 위치에서의 특정 아미노산 잔기 차이는 "XnY"로 표시되고, 여기서 "Xn"은 상기 기술된 바와 같이 상응하는 위치를 명시하고, "Y"는 조작된 폴리펩티드에서 발견되는 아미노산의 단일 문자 식별자이다(즉, 참조 폴리펩티드 중의 것과 다른 잔기). 일부 경우에서, 본 개시내용은 또한 통상의 표기법 "AnB"로 표시된 특정 아미노산 차이를 제공하고, 여기서, A는 참조 서열 중의 잔기의 단일 문자 식별자이고, "n"은 참조 서열 중의 잔기 위치의 번호이고, B는 조작된 폴리펩티드의 서열 중의 잔기 치환의 단일 문자 식별자이다. 일부 경우에서, 본 개시내용의 폴리펩티드는 잔기 차이가 참조 서열 대비로 존재하는 명시된 위치의 목록으로 표시되는, 참조 서열 대비의 하나 이상의 아미노산 잔기 차이를 포함할 수 있다. 일부 실시양태에서, 1 초과의 아미노산이 폴리펩티드의 특정 잔기 위치에 사용될 수 있는 경우, 사용될 수 있는 다양한 아미노산 잔기는 "/"로 분리되어 표시된다(예컨대, X192A/G). 일부 실시양태에서, 치환 세트 중의 치환은 세미콜론(";") 또는 슬래시("/")로 분리되어 표시된다(예컨대, 서열 번호: 8 대비 하기 치환 세트--Y27T;G71H;D74G;D484N;Q547K;Y584F;M697L을 가지는 변이체 PGA 경우). 본 개시내용은 보존적 및 비보존적 아미노산 치환 중 하나 또는 그 둘 모두를 포함하는 하나 이상의 아미노산 차이를 포함하는 조작된 폴리펩티드 서열을 포함한다. 본 개시내용의 서열 목록에 포함되는 특정 재조합 카보닉 안히드라제 폴리펩티드의 아미노산 서열은 개시 메티오닌(M) 잔기(즉, M은 잔기 위치 1을 나타낸다)를 포함한다. 그러나, 당업자는 이러한 개시 메티오닌 잔기가 생물학적 프로세싱 조구, 예컨대, 숙주 세포 또는 시험관내 번역 시스템에서 제거됨으로써 개시 메티오닌 잔기가 결여되지만, 효소의 특성은 유지되는 성숙한 단백질이 생성될 수 있다는 것을 이해한다. 결과적으로, 본원에서 사용되는 바, "서열 번호: 2 대비 위치 Xn에서의 아밈노산 잔기 차이"라는 용어는 위치 "Xn" 또는 출발 메티오닌을 결여시키도록 프로세싱된 참조 서열 중의 상응하는 위치(예컨대, 위치(X-1)n)를 의미할 수 있다.

[0086] 본원에서 사용되는 바, "보존적 아미노산 치환"이라는 어구는 유사한 측쇄를 가지는 잔기의 상호교환성을 지칭하고, 따라서, 이는 전형적으로 폴리펩티드 중의 아미노산을 동일하거나 또는 유사한 것으로 정의된 부류의 아미노산 내의 아미노산으로 치환하는 것을 포함한다. 예로서 및 제한 없이, 일부 실시양태에서, 지방족 측쇄를 가지는 아미노산은 또 다른 지방족 아미노산(예컨대, 알라닌, 발린, 류신, 및 이소류신)으로 치환되고/거나; 히드록실 측쇄를 가지는 아미노산은 히드록실 측쇄를 가지는 또 다른 아미노산(예컨대, 세린 및 트레오닌)으로 치환되고/거나; 방향족 측쇄를 가지는 아미노산은 방향족 측쇄를 가지는 또 다른 아미노산(예컨대, 페닐알라닌, 티로신, 트립토판, 및 히스티딘)으로 치환되고/거나; 염기성 측쇄를 가지는 아미노산은 염기성 측쇄를 가지는 또 다른 아미노산(예컨대, 리신 및 아르기닌)으로 치환되고/거나; 산성 측쇄를 가지는 아미노산은 산성 측쇄를 가지는 또 다른 아미노산(예컨대, 아스파르트산 또는 글루탐산)으로 치환되고/거나; 소수성 또는 친수성 아미노산은 각각 또 다른 소수성 또는 친수성 아미노산으로 대체된다. 예시적인 보존적 치환은 표 1에 제공되어 있다.

표 1

예시적인 보존적 아미노산 치환	
잔기	잠재적인 보존적 치환
A, L, V, I	다른 지방족 (A, L, V, I) 다른 비극성 (A, L, V, I, G, M)
G, M	다른 비극성 (A, L, V, I, G, M)
D, E	다른 산성 (D, E)
K, R	다른 염기성 (K, R)
N, Q, S, T	다른 극성
H, Y, W, F	다른 방향족 (H, Y, W, F)
C, P	비극성

[0087]

[0088] 본원에서 사용되는 바, "비보존적 치환"이라는 어구는 폴리펩티드 중의 아미노산을, 유의적으로 상이한 다른 측쇄 특성을 가지는 아미노산으로 치환하는 것을 지칭한다. 비보존적 치환은 정의된 군 안에서 보다는, 그 사이의 아미노산을 사용할 수 있고, (a) 치환 영역 내 펩티드 골격의 구조(예컨대, 글리신 대신 프롤린), (b) 전하 또는 소수성, 또는 (c) 측쇄의 부피에 영향을 준다. 예로서 및 제한 없이, 예시적인 비보존적 치환은 염기성 또는 지방족 아미노산으로 치환된 산성 아미노산, 소형 아미노산으로 치환된 방향족 아미노산, 및 소수성 아미노산으로 치환된 친수성 아미노산일 수 있다.

[0089] 본원에서 사용되는 바, "결실"은 참조 폴리펩티드로부터의 하나 이상의 아미노산의 제거에 의한 폴리펩티드의 변형을 지칭한다. 결실은 효소 활성은 유지하고/거나, 조작된 효소의 개선된 특성은 유지하면서, 1개 이상의 아미노산, 2개 이상의 아미노산, 5개 이상의 아미노산, 10개 이상의 아미노산, 15개 이상의 아미노산, 또는 20개 이상의 아미노산, 아미노산 총 개수의 최대 10%, 또는 폴리펩티드를 구성하는 아미노산의 총 개수의 최대 20%의 제거를 포함할 수 있다. 결실은 폴리펩티드의 내부 부분 및/또는 말단 부분으로 지정될 수 있다. 다양한 실시양태에서, 결실은 연속되는 세그먼트를 포함할 수 있거나, 또는 비연속적일 수 있다.

[0090] 본원에서 사용되는 바, "삽입"은 하나 이상의 아미노산의 참조 폴리펩티드에의 부가에 의한 폴리펩티드의 변형을 지칭한다. 일부 실시양태에서, 개선된 조작된 PGA 효소는 하나 이상의 아미노산의 자연적으로 발생된 PGA 폴리펩티드에의 삽입 뿐만 아니라, 하나 이상의 아미노산의 조작된 PGA 폴리펩티드에의 삽입을 포함한다. 삽입은 폴리펩티드의 내부 부분에 있을 수 있거나, 또는 카복시 또는 아미노 말단에 이루어질 수 있다. 본원에서 사용되는 바, 삽입은 당업계에 공지된 바와 같은 융합 단백질을 포함한다. 삽입부는 아미노산의 인접한 세그먼트일 수 있거나, 또는 자연적으로 발생된 폴리펩티드 중의 아미노산의 하나 이상의 것에 의해 이격되어 있을 수 있다.

[0091] "아미노산 치환 세트" 또는 "치환 세트"라는 용어는 참조 서열과 비교하여, 폴리펩티드 서열 중의 아미노산 치환 군을 지칭한다. 치환 세트는 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15개 이상의 아미노산 치환을 가질 수 있다. 일부 실시양태에서, 치환 세트는 실시예에 제공된 표에 열거된 변이체 PGA 중 임의의 것에 존재하는 아미노산 치환 세트를 지칭한다.

[0092] 본원에서 사용되는 바, "단편"은 아미노 말단 및/또는 카복시 말단 결실을 가지지만, 나머지 아미노산 서열은 서열 중의 상응하는 위치와 동일한 폴리펩티드를 지칭한다. 단편은 전형적으로, 전장의 PGA 폴리펩티드, 예를 들어, 서열 번호: 2의 폴리펩티드의 약 80%, 약 90%, 약 95%, 약 98%, 또는 약 99%를 가질 수 있다. 일부 실시양태에서, 단편은 "생물학적으로 활성"이다(즉, 전장의 서열과 동일한 효소 활성을 나타낸다).

[0093] 본원에서 사용되는 바, "단리된 폴리펩티드"는 그와 자연적으로 동반되는 다른 오염물질, 예컨대, 단백질, 지질 및 폴리뉴클레오티드로부터 실질적으로 분리된 폴리펩티드를 지칭한다. 상기 용어는 그의 자연적으로 발생된 환경 또는 발생 시스템(예컨대, 숙주 세포 또는 시험관내 합성)으로부터 제거되거나, 또는 정제된 폴리펩티드를

포함한다. 개선된 PGA 효소는 세포 내에 존재하거나, 세포 매질에 존재하거나, 또는 다양한 형태, 예컨대, 용해물 또는 단리된 제제로 제조될 수 있다. 따라서, 일부 실시양태에서, 본 개시내용의 조작된 PGA 폴리펩티드는 단리된 폴리펩티드일 수 있다.

[0094] 본원에서 사용되는 바, "실질적으로 순수한 폴리펩티드"는 그 폴리펩티드 종이 존재하는 우세한 종인(즉, 몰 농도 또는 중량 기준으로 조성물 중 임의의 다른 개별 거대 분자 종보다 더 풍부한) 조성물을 의미하고, 대상 종이 존재하는 거대 분자 종의 적어도 약 50%(몰 농도 또는 중량% 기준)를 포함할 때 일반적으로 실질적으로 정제된 조성물이다. 일반적으로, 실질적으로 순수한 조작된 PGA 폴리펩티드 조성물은 조성물에 존재하는 모든 거대 분자 종의 약 60% 이상, 약 70% 이상, 약 80% 이상, 약 90% 이상, 약 91% 이상, 약 92% 이상, 약 93% 이상, 약 94% 이상, 약 95% 이상, 약 96% 이상, 약 97% 이상, 약 98% 이상, 또는 약 99%(몰 농도 또는 중량% 기준)를 포함한다. 용매 종, 소형 분자(< 500 달톤), 및 원소 이온 종은 거대분자 종으로 간주되지 않는다. 일부 실시양태에서, 단리된 개선된 PGA 폴리펩티드는 실질적으로 순수한 폴리펩티드 조성물이다.

[0095] 본원에서 사용되는 바, 핵산 또는 폴리펩티드와 관련하여 사용될 때, "이종성"이라는 용어는 유기체(예컨대, 야생형 유기체)에 의해 정상적으로 발현 및 분비되지 않는 서열을 지칭한다. 일부 실시양태에서, 상기 용어는 자연계에서 보통 발견되는 것과 서로 동일한 관계로 발견되지 않는 2 이상의 서브서열을 포함하거나, 또는 재조합적으로 조작되어 그의 발현 수준, 또는 세포 내에서의 다른 핵산 또는 다른 분자와의 물리적 관계, 또는 구조가 자연계에서 보통 발견되지 않는 서열을 포함한다. 예를 들어, 자연계에서 발견되지 않는 방식으로 배열된 비관련 유전자로부터의 2개 이상의 서열을 가지는 이종성 핵산은 전형적으로 재조합적으로 제조된다(예컨대, 발현 카세트, 예컨대, 벡터에 삽입된 프로모터 서열에 작동적으로 연결된 본 발명의 핵산 오픈 리딩 프레임(ORF: open reading frame)). 일부 실시양태에서, "이종성 폴리뉴클레오티드"는 실험실 기술에 의해 숙주 세포에 도입된 임의의 폴리뉴클레오티드를 지칭하고, 숙주 세포로부터 제거되고, 실험실 조작된 후, 이어서, 숙주 세포 내로 재도입된 폴리뉴클레오티드를 포함한다.

[0096] 본원에서 사용되는 바, "적합한 반응 조건"은 본 개시내용의 PGA 폴리펩티드가 트리-페닐 아세테이트 보호기를 제거함으로써 유리 인슐린을 방출할 수 있는 생물촉매 반응 용액 중의 조건(예컨대, 효소 적재량, 기질 적재량, 보조인자 적재량, 온도, pH, 완충액, 공용매 등의 범위)을 의미한다. 예시적인 "적합한 반응 조건"은 본 개시내용에 제공되어 있고, 실시예에 의해 예시된다.

[0097] 본원에서 사용되는 바, 예컨대, "화합물 적재량," "효소 적재량," "보조인자 적재량"에서 "적재량"은 반응의 출발시 반응 혼합물 중 성분의 농도 또는 양을 의미한다.

[0098] 본원에서 사용되는 바, 생물촉매 매개 프로세스에서 "기질"은 생물촉매에 의한 작용을 받는 화합물 또는 분자를 지칭한다.

[0099] 본원에서 사용되는 바, 생물촉매 매개 프로세스에서 "생성물"은 생물촉매의 작용 결과에 의한 화합물 또는 분자를 지칭한다.

[0100] 본원에서 사용되는 바, "평형"은 본원에서 사용되는 바, 화학 또는 효소 반응의 정반응 속도 상수 및 역반응 속도 상수로 측정되는 바와 같은, 입체이성질체의 상호전환을 포함하는, 화학 또는 효소 반응(예컨대, 2개 종 A 및 B의 상호전환)의 화학 종의 정상 상태 농도를 야기시키는 프로세스를 의미한다.

[0101] 본원에서 사용되는 바 "아실라제" 및 "아실트랜스퍼라제"는 상호교환적으로 사용되며, 이는 아실 기를 공여자에서 수용자에게로 전달하여 에스테르 또는 아미드를 형성할 수 있는 효소를 지칭한다. 아실라제 매개 역반응은 에스테르 또는 아미드의 가수분해를 일으킨다.

[0102] 본원에서 사용되는 바, "페니실린 G" 및 "벤질페니실린"이란, (2S,5R,6R)-3,3-디메틸-7-옥소-6-(2-페닐아세트아미도)-4-티아-1-아자비사이클로[3.2.0]헵탄-2-카복실산($C_{16}H_{18}N_2O_4S$)으로도 공지되어 있는 항생제를 지칭한다. 비록 일부 그람 음성 유기체 또한 이에 감수성이기는 하지만, 이는 주로 그람 양성 유기체에 효과적이다.

[0103] 본원에서 사용되는 바, "페니실린 G 아실라제" 및 "PGA"는 상호교환적으로 사용되며, 이는 페니실린 G(벤질페니실린)의 페닐아세트산(PHA) 및 6-아미노페니실란산(6-APA)으로의 절단을 매개할 수 있는 능력을 가진 효소를 지칭한다. 일부 실시양태에서, PGA 활성은 모델 기질의 절단, 예를 들어, 6-니트로-3-(페닐아세트아미드)벤조산의 페닐아세트산 및 5-아미노-2-니트로-벤조산으로의 절단을 기초로 할 수 있다. PGA는 또한 아실 공여자의 아실 기를 아실 수용자에게로 전달하는 역반응을 수행할 수 있다. 본원에서 사용되는 바, PGA는 자연적으로 발생된 (야생형) PGA 뿐만 아니라, 인간 조작에 의해 생성된 하나 이상의 조작된 폴리펩티드를 포함하는 비자연적으로

발생된 PGA 효소도 포함한다. 야생형 PGA 유전자는 54개의 아미노산으로 이루어진 스페이서 영역에 의해 연결된 알파 서브유니트(23.8 KDa) 및 베타 서브유니트(62.2 KDa)으로 구성된 이종이량체이다. 스페이서 영역이 존재하기 때문에, 활성 단백질을 형성하는 데 자가 프로세싱 단계가 요구된다.

[0104] 본원에서 사용되는 바, "아실 공여자"는 아실 기를 아실 수용자에 제공하여 에스테르 또는 아미드를 형성하는 아실라제 기질의 일부를 지칭한다.

[0105] 본원에서 사용되는 바, "아실 수용자"는 아실 공여자의 아실 기를 수용하여 에스테르 또는 아미드를 형성하는 아실라제 기질의 일부를 지칭한다.

[0106] 본원에서 사용되는 바, "α 쇄 서열"은 서열 번호: 2의 27 내지 235번 위치에 있는 잔기에 상응하는(예컨대, 상기 잔기와 적어도 85%의 동일성을 가지는) 아미노산 서열을 지칭한다. 본원에서 사용되는 바, 단일 쇄 폴리펩티드는 "α 쇄 서열" 및 추가 서열(들)을 포함할 수 있다.

[0107] 본원에서 사용되는 바, "β 쇄 서열"은 서열 번호: 2의 290 내지 846번 위치에 있는 잔기에 상응하는(예컨대, 상기 잔기와 적어도 85%의 동일성을 가지는) 아미노산 서열을 지칭한다. 본원에서 사용되는 바, 단일 쇄 폴리펩티드는 "β 쇄 서열" 및 추가 서열(들)을 포함할 수 있다.

[0108] 본원에서 사용되는 바, 조작된 PGA 효소와 관련하여 사용될 때, "~로부터 유도된"은 조작의 기반이 된 원래의 PGA 효소, 및/또는 상기 PGA 효소를 코딩하는 유전자를 구별짓는다. 예를 들어, 서열번호 60의 조작된 PGA 효소는 다세대에 걸쳐 서열 번호: 2의 K. 시트로필라(*K. citrophila*) PGA 알파 쇄 및 베타 쇄를 코딩하는 유전자를 인공적으로 진화시킴으로써 수득되었다. 따라서, 상기 조작된 PGA 효소는 자연적으로 발생된 또는 야생형 PGA"로부터 유도된" 것이다.

[0109] 본원에서 사용되는 바, "인슐린"은 정상 개체 내 췌장의 베타 세포에 의해 생산되는 폴리펩티드 호르몬을 지칭한다. 인슐린은 혈당 수준을 감소시킴으로써, 탄수화물 물질대사를 조절하는 데 필수적이다. 인슐린의 전신 결핍은 당뇨병을 유발한다. 인슐린은 51개의 아미노산으로 구성되고, 분자량은 대략 5800 달톤이다. 인슐린은 하나의 서브유니트내 이황화 결합 및 2개의 서브유니트간 이황화 결합을 함유하는, 2개의 펩티드 쇄("A" 및 "B"로 명명)로 구성된다. A 쇄는 21개의 아미노산으로 구성되고, B 쇄는 30개의 아미노산으로 구성된다. 2개 쇄는 고도로 정돈된 구조를 형성하고, A 및 B 쇄, 둘 모두에 수개의 알파 나선 영역이 존재한다. 단리된 쇄은 불활성이다. 용액에서, 인슐린은 단량체, 이량체 또는 육량체이다. 피하 주사에 사용되는 고농축 제제 중에서는 육량체이지만, 체액에 희석되면서 단량체가 된다. 이 정의는 1차 구조적 입체형태의 일부 또는 모두 및 자연적으로 발생된 인슐린의 생물학적 특성 중 적어도 하나를 가지는 임의의 정제된 단리된 폴리펩티드 및 프로인슐린을 포함하는 것으로 의도된다. 당형태 뿐만 아니라, 유사체(예컨대, 결실, 삽입 및/또는 치환을 가지는 폴리펩티드)를 비롯한, 천연 및 합성 유도된 인슐린을 포함하는 것으로 추가로 의도된다.

[0110] 인슐린은 페닐아세테이트 공여자와 잠재적으로 반응할 수 있고, PGA에 의해 탈보호화될 수 있는 3개의 친핵성 아민을 함유한다. 이들 잔기는 29번 위치의 B쇄(B29) 상의 Lys 및 2개 N 말단 유리 아민, 1번 위치의 A 쇄(A1) 상의 Gly 및 1범 위치의 B 쇄(B1) 상의 Phe를 포함한다. 본원에서는 삼중 보호된 인슐린(인간 인슐린 상의 A1, B1, B29 잔기에 화학적으로 부착된 페닐 아세테이트)을 제공한다. PGA는 페닐아세테이트 아미드 결합에 대한 배타적인 선택성으로, 단백질의 펩티드 결합의 나머지는 온전하게 남겨두고, N-페닐아세테이트 보호된 펩티드 및 인슐린의 가수분해를 촉매화시키는 것으로 보고되었다(문헌 [Brtnik et al., Coll. Czech. Chem. Commun., 46 (8), 1983-1989 [1981]]; 및 [Wang et al. Biopolym., 25 (Suppl.), S109-S114 [1986]]).

[0111] 본원에서 사용되는 바, "트리-페닐 아세테이트 보호기"란, 페닐 아실 기로 보호된 B1, B29 및 A1 위치에 3개의 1급 아민을 가지는 인슐린 분자를 지칭한다.

[0112] 본원에서 사용되는 바, "디-페닐 아세테이트 보호기"란, 페닐 아실 기로 보호된 B1, B29 및/또는 A1 위치에 2개의 1급 아민을 가지는 인슐린 분자를 지칭한다.

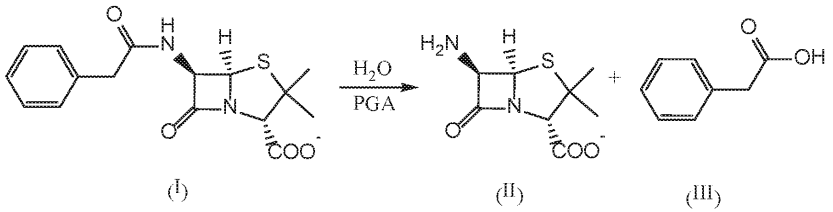
[0113] 본원에서 사용되는 바, "디-페닐 아세테이트 보호기"란, 페닐 아실 기로 보호된 B1, B29 또는 A1 위치에 1개의 1급 아민을 가지는 인슐린 분자를 지칭한다.

[0114] **페니실린 G 아실라제**

[0115] 페니실린 아실라제는 (Sakaguchi 및 Murao) (문헌 [Sakaguchi and Murao, J. Agr.Chem. Soc. Jpn., 23:411 [1950]])에 의해 페니실리움 크리소게눔(*Penicillium chrysogenum*) Wisc. Q176으로부터 최초로 기술되었다. 페니실린 G 아실라제는 페니실린 G, 세팔로스포린 G, 및 관련 항생제의 측쇄에 작용하여 β 락탐 항생제 중간체인

6-아미노 페니실란산 및 7-아미노 데스-아세톡시 세팔로스포란산과 공통 부산물로서 페닐 아세트산을 생산하는 가수분해 효소이다. 이들 항생제 중간체는 반합성 항생제, 예컨대, 암피실린, 아목시실린, 클록사실린, 세팔렉신, 및 세파톡심의 잠재적인 빌딩 블록 중 하나이다.

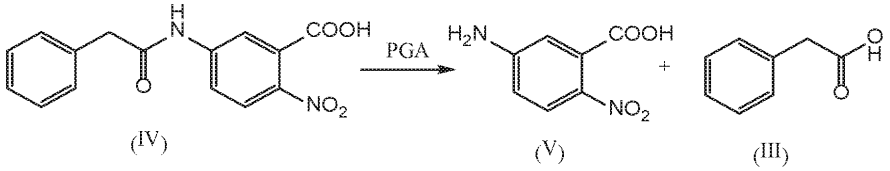
[0116] 상기 명시된 바와 같이, 페니실린 G 아실라제(PGA)는 반응식 1에 제시된 바와 같이, 구조식(I)의 짝염기를 가지는 페니실린 G의 구조식(II)의 짝염기를 가지는 6-아미노 페니실란산, 및 구조식(III)의 페닐아세트산으로의 가수분해적 절단을 촉매화할 수 있는 능력을 특징으로 한다:



반응식 1

[0117]

[0118] 이론에 의해 제한되지 않지만, 기질 특이성은 소수성 페닐 기의 인식과 연관이 있는 것으로 보이는 반면, 일부 PGA에서 베타 쇄의 N 말단의 세린 잔기인 친핵체는 베타 락탐 및 다양한 다른 기, 예컨대, 베타 아미노산의 수용자로서 작용한다. PGA는 또한 페니실린 G와 유사한 모델 기질을 절단하는 능력, 예를 들어, 반응식 2에 제시된 바와 같이, 구조식(IV)의 6-니트로-3-(페닐아세트아미도)벤조산(NIPAB)을 구조식(III)의 페닐아세트산 및 구조식(V)의 5-아미노-2-니트로-벤조산으로 절단할 수 있는 능력을 특징으로 할 수 있다(문헌 [Alkema et al., Anal. Biochem., 275:47-53 [1999]] 참조):



반응식 2

[0119]

[0120] 5-아미노-2-니트로-벤조산은 발색성을 띠기 때문에, 화학식(IV)의 기질은 PGA 활성을 측정하는 편리한 방식을 제공한다. 상기 반응 이외에도, PGA는 또한 광학적으로 순수한 tert 류신의 제조를 위한 DL-tert 류신의 동적 분할에도 사용될 수 있다(예컨대, 문헌 [Liu et al., Prep. Biochem. Biotechnol., 36:235-41 [2006]] 참조).

[0121] 본 개시내용의의 PGA는 유기체 클루이베라 시트로필라(K. 시트로필라)로부터 수득된 효소를 기반으로 한다. 다른 유기체 유래의 PGA와 같이, K. 시트로필라의 PGA는 프리-프로-PGA 폴리펩티드의 단백질가수분해 프로세싱에 의해 생성되는 알파 서브유니트 및 베타 서브유니트로 구성된 이종이량체 효소이다. 신호 펩티드 및 스페이서 펩티드를 제거하면, 성숙한 이종이량체가 생성된다(예컨대, 문헌 [Barbero et al., Gene 49:69-80 [1986]] 참조). K. 시트로필라의 자연적으로 발생된 프리-프로-PGA 폴리펩티드의 아미노산 서열은 공개적으로 이용가능하고(예컨대, 진뱅크(Genbank) 수탁 번호 P07941, [gi:129551]), 이는 본원에서 서열 번호: 2로 제공된다. 자연적으로 발생된 K. 시트로필라 PGA의 알파 쇄 서열은 서열 번호: 2의 잔기 27 내지 235에 상응한다. 자연적으로 발생된 K. 시트로필라 PGA의 베타 쇄 서열은 서열 번호: 2의 잔기 290 내지 846에 상응한다. 서열 번호: 2의 잔기 1 내지 26은 신호 펩티드에 상응하고 서열 번호: 2의 잔기 236-289는 연결 프로펩티드에 상응하며, 둘 모두는 제거되어 α 쇄 서브유니트 및 β 쇄 서브유니트를 포함하는 이종이량체인 자연적으로 발생된 성숙한 PGA 효소를 생성한다.

[0122] 일부 실시양태에서, 본 발명은 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 약 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 또는 99% 또는 그 이상의 서열 동일성을 가지는 아미노산 서열을 포함하는 조작된 PGA 폴리펩티드를 제공한다.

[0123] 본 발명은 상업적 규모의 용도에 적합한 인슐린 특이적 탈아실화 생물촉매를 제공한다. 유도 진화는 A1/B1/B29-트리-페닐 아세테이트 보호기를 제거하거나, 또는 그를 인슐린에 부가할 수 있는 효율적인 아실라제 변이체를 개발하는 데 사용되었다. 본원에 제공된 PGA 변이체는 매우 다양한 아실기를 수용할 수 있고, 야생형 PGA와 비교하여, 증가된 용매 안정성, 및 개선된 열 안정성을 나타낸다. 본원에 제공된 변이체 PGA는 스페이서 영역이

없다. 따라서, 활성 효소 생성을 위한 자가 프로세싱 단계가 요구되지 않는다.

[0124] 본 발명은 또한 조작된 PGA 폴리펩티드를 코딩하는 폴리뉴클레오티드를 제공한다. 일부 실시양태에서, 폴리뉴클레오티드는 유전자 발현을 제어하는 하나 이상의 이종성 조절 서열에 작동적으로 연결되어 있고, 이로써, 폴리펩티드를 발현할 수 있는 재조합 폴리뉴클레오티드가 생성된다. 조작된 PGA 폴리펩티드를 코딩하는 이종성 폴리뉴클레오티드를 함유하는 발현 구성물은 적절한 숙주 세포 내로 도입되어 상응하는 PGA 폴리펩티드를 발현할 수 있다.

[0125] 다양한 아미노산에 상응하는 코돈에 관한 지식에 기인하여, 단백질 서열의 이용가능성이 대상을 코딩할 수 있는 모든 폴리뉴클레오티드에 관한 설명을 제공한다. 동일한 아미노산을 대안적 또는 동의 코돈에 의해 코딩하는 유전자 코드의 축퇴성을 통해, 모두가 본원에 개시된 개선된 PGA 효소를 코딩하는 것인, 매우 많은 핵산을 제조할 수 있다. 따라서, 특정 아미노산 서열을 확인함으로써, 당업자는 단백질의 아미노산 서열을 변이시키지 않는 방식으로 하나 이상의 코돈의 서열을 단순하게 변형시킴으로써 임의 개수의 상이한 핵산을 제조할 수 있다. 이와 관련하여, 본 개시내용은 구체적으로 가능한 코돈 선택을 기반으로 조합을 선택함으로써 제조될 수 있는 각각의 모든 가능한 폴리뉴클레오티드의 변이를 고려하고, 상기의 모든 변이는 실시예 5 및 6의 표에 제시된 아미노산 서열을 비롯한, 본원에 개시된 임의의 폴리펩티드에 대해 구체적으로 개시된 것으로 간주되어야 한다.

[0126] 다양한 실시양태에서, 코돈은 바람직하게 단백질이 제조되는 숙주 세포에 적합하도록 선택된다. 예를 들어, 박테리아에서의 사용에 바람직한 코돈은 박테리아에서 유전자를 발현하는 데 사용되고, 효모에서의 사용에 바람직한 코돈은 효모에서의 발현을 위해 사용되고; 포유동물에서의 사용에 바람직한 코돈은 포유동물 세포에서의 발현을 위해 사용된다.

[0127] 특정 실시양태에서, 천연 서열이 바람직한 코돈을 포함하게 되고, 바람직한 코돈의 사용이 모든 아미노산 잔기에 필요하지 않을 수 있기 때문에, PGA 폴리펩티드의 코돈 용법을 최적화하기 위해 모든 코돈이 교체될 필요는 없다. 결과적으로, PGA 효소를 코딩하는 코돈 최적화된 폴리뉴클레오티드는 전장의 코딩 영역의 코돈 위치의 약 40%, 50%, 60%, 70%, 80%로, 또는 90% 초과로 바람직한 코돈을 함유할 수 있다.

[0128] 일부 실시양태에서, 폴리뉴클레오티드는 본원에 기술된 참조 조작된 PGA 폴리펩티드 중 임의의 것의 알파 쇄 및/또는 베타 쇄와 적어도 약 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 또는 99% 또는 그 이상의 서열 동일성을 가지는 아미노산 서열을 포함하는 PGA 폴리펩티드를 코딩하는 뉴클레오티드 서열을 포함한다. 따라서, 일부 실시양태에서, 폴리뉴클레오티드는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288에 기반한 참조 알파 및 베타 쇄 서열과 적어도 약 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 아미노산 서열을 코딩한다. 일부 실시양태에서, 폴리뉴클레오티드는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288의 알파 및/또는 베타 쇄 아미노산 서열을 코딩한다.

[0129] 일부 실시양태에서, 폴리뉴클레오티드는 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및 1288과 적어도 약 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 또는 99% 또는 그 이상의 서열 동일성을 가지는 아미노산 서열을 포함하는 PGA 폴리펩티드를 코딩하는 뉴클레오티드 서열을 포함한다. 따라서, 일부 실시양태에서, 폴리뉴클레오티드는 서열 번호: 3, 7, 13, 299, 1035, 1193, 1261, 및 1287과 적어도 약 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 또는 그 이상 동일한 아미노산 서열을 코딩한다.

[0130] 일부 실시양태에서, 개선된 PGA 폴리펩티드를 코딩하는 단리된 폴리뉴클레오티드는 폴리펩티드의 개선된 활성 및/또는 발현을 제공하는 다양한 방식으로 조작되었다. 단리된 폴리뉴클레오티드의 벡터 내로의 삽입 이전에 그를 조작하는 것이 발현 벡터에 따라 바람직하거나, 또는 필요할 수 있다. 재조합 DNA 방법을 이용하여 폴리뉴클레오티드 및 핵산 서열을 변형시키는 방법은 당업계에 널리 공지되어 있다.

[0131] 예를 들어, 돌연변이유발법 및 유도 진화 방법은 폴리뉴클레오티드에 쉽게 적용될 수 있고, 이로써, 발현, 스크리닝, 검정될 수 있는 변이체 라이브러리를 생성할 수 있다. 돌연변이유발법 및 유도 진화 방법은 당업계에 널리 공지되어 있다(예컨대, 미국 특허 번호 5,605,793, 5,811,238, 5,830,721, 5,834,252, 5,837,458, 5,928,905, 6,096,548, 6,117,679, 6,132,970, 6,165,793, 6,180,406, 6,251,674, 6,265,201, 6,277,638, 6,287,861, 6,287,862, 6,291,242, 6,297,053, 6,303,344, 6,309,883, 6,319,713, 6,319,714, 6,323,030, 6,326,204, 6,335,160, 6,335,198, 6,344,356, 6,352,859, 6,355,484, 6,358,740, 6,358,742, 6,365,377, 6,365,408, 6,368,861, 6,372,497, 6,337,186, 6,376,246, 6,379,964, 6,387,702, 6,391,552, 6,391,640,

6,395,547, 6,406,855, 6,406,910, 6,413,745, 6,413,774, 6,420,175, 6,423,542, 6,426,224, 6,436,675, 6,444,468, 6,455,253, 6,479,652, 6,482,647, 6,483,011, 6,484,105, 6,489,146, 6,500,617, 6,500,639, 6,506,602, 6,506,603, 6,518,065, 6,519,065, 6,521,453, 6,528,311, 6,537,746, 6,573,098, 6,576,467, 6,579,678, 6,586,182, 6,602,986, 6,605,430, 6,613,514, 6,653,072, 6,686,515, 6,703,240, 6,716,631, 6,825,001, 6,902,922, 6,917,882, 6,946,296, 6,961,664, 6,995,017, 7,024,312, 7,058,515, 7,105,297, 7,148,054, 7,220,566, 7,288,375, 7,384,387, 7,421,347, 7,430,477, 7,462,469, 7,534,564, 7,620,500, 7,620,502, 7,629,170, 7,702,464, 7,747,391, 7,747,393, 7,751,986, 7,776,598, 7,783,428, 7,795,030, 7,853,410, 7,868,138, 7,783,428, 7,873,477, 7,873,499, 7,904,249, 7,957,912, 7,981,614, 8,014,961, 8,029,988, 8,048,674, 8,058,001, 8,076,138, 8,108,150, 8,170,806, 8,224,580, 8,377,681, 8,383,346, 8,457,903, 8,504,498, 8,589,085, 8,762,066, 8,768,871, 9,593,326, 및 모든 관련 PCT 및 US 이외의 대응 특허; [Ling et al., Anal. Biochem., 254(2):157-78 [1997]]; [Dale et al., Meth. Mol. Biol., 57:369-74 [1996]]; [Smith, Ann. Rev. Genet., 19:423-462 [1985]]; [Botstein et al., Science, 229:1193-1201 [1985]]; [Carter, Biochem. J., 237:1-7 [1986]]; [Kramer et al., Cell, 38:879-887 [1984]]; [Wells et al., Gene, 34:315-323 [1985]]; [Minshull et al., Curr. Op. Chem. Biol., 3:284-290 [1999]]; [Christians et al., Nat. Biotechnol., 17:259-264 [1999]]; [Crameri et al., Nature, 391:288-291 [1998]]; [Crameri, et al., Nat. Biotechnol., 15:436-438 [1997]]; [Zhang et al., Proc. Nat. Acad. Sci. U.S.A., 94:4504-4509 [1997]]; [Crameri et al., Nat. Biotechnol., 14:315-319 [1996]]; [Stemmer, Nature, 370:389-391 [1994]]; [Stemmer, Proc. Nat. Acad. Sci. USA, 91:10747-10751 [1994]]; WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; WO 01/75767; 및 WO 2009/152336(상기 문헌들은 모두 본원에서 참조로 포함된다) 참조).

[0132] 일부 실시양태에서, 본 발명의 변이체 PGA 아실라제는 효소의 코딩된 활성을 변경시키지 않는 추가 서열을 추가로 포함한다. 예를 들어, 일부 실시양태에서, 변이체 PGA 아실라제는 정제에 유용한 또 다른 서열 또는 에피토프 태그에 연결된다.

[0133] 일부 실시양태에서, 본 발명의 변이체 PGA 아실라제 폴리펩티드는 그들이 발현되는 숙주 세포(예컨대, 효모 또는 섬유상 진균 숙주 세포)에서 분비되고, 신호 펩티드(즉, 폴리펩티드의 아미노 말단에 연결되고, 코딩된 폴리펩티드를 세포 분비 경로로 유도하는 아미노산 서열)을 포함한 프리-단백질로서 발현된다.

[0134] 일부 실시양태에서, 신호 펩티드는 내인성 K. 시트로필라 PGA 아실라제 신호 펩티드이다. 일부 다른 실시양태에서, 다른 K. 시트로필라 분비 단백질로부터의 신호 펩티드가 사용된다. 일부 실시양태에서, 다른 신호 펩티드가 숙주 세포 및 다른 인자들에 의존적으로 사용된다. 섬유상 진균 숙주 세포에 효과적인 신호 펩티드 코딩 영역으로는 아스퍼질러스 오리재(*Aspergillus oryzae*) TAKA 아밀라제, 아스퍼질러스 니거(*Aspergillus niger*) 중성 아밀라제, 아스퍼질러스 니거 글루코아밀라제, 리조무코르 미에헤이(*Rhizomucor miehei*) 아스파르트산 프로테이나제, 휴미콜라 인솔렌스(*Humicola insolens*) 셀룰라제, 휴미콜라 라누기노사(*Humicola lanuginosa*) 리파제, 티. 리에세이(*T. reesei*) 셀로비오히드롤라제 II로부터 수득된 신호 펩티드 코딩 영역을 포함하나, 이에 제한되지 않는다. 박테리아 숙주 세포에 대한 신호 펩티드 코딩 영역으로는 바실러스(*Bacillus*) NClB 11837 말토스형성 아밀라제, 바실러스 스테아로써모필러스(*Bacillus stearothermophilus*) 알파 아밀라제, 바실러스 리체니포르미스(*Bacillus licheniformis*) 섭틸리신, 바실러스 리체니포르미스 β-락타마제, 바실러스 스테아로써모필러스 중성 프로테아제(nprT, nprS, nprM), 및 바실러스 섭틸리스(*Bacillus subtilis*) prsA에 대한 유전자로부터 수득된 신호 펩티드 코딩 영역을 포함하나, 이에 제한되지 않는다. 일부 추가의 실시양태에서, 다른 신호 펩티드가 본 발명에서 사용된다(예컨대, 문헌 [Simonen and Palva, Microbiol. Rev., 57: 109-137 [1993](본원에서 참조로 포함된다) 참조). 효모 숙주 세포에 대해 추가로 유용한 신호 펩티드는 사카로마이세스 세레비지아에(*Saccharomyces cerevisiae*) 알파 인자, 사카로마이세스 세레비지아에 SUC2 인버타제에 대한 유전자로부터의 것을 포함한다(예컨대, 문헌 [Taussig and Carlson, Nucl. Acids Res., 11:1943-54 [1983]]; 스위스프로트(SwissProt) 수탁 번호 P00724; 및 [Romanos *et al.*, Yeast 8:423-488 [1992]] 참조). 일부 실시양태에서, 이들 신호 펩티드 및 다른 신호 펩티드의 변이체가 사용된다. 실제로, 본 발명은 당업계에 공지된 임의의 적합한 신호 펩티드가 본 발명에서 사용되는 바, 임의의 특정 신호 펩티드로 제한되는 것으로 의도되지 않는다.

[0135] 일부 실시양태에서, 본 발명은 본원에 기술된 바와 같이, 변이체 PGA 아실라제 폴리펩티드, 및/또는 그의 생물학적 활성 단편을 코딩하는 폴리뉴클레오티드를 제공한다. 일부 실시양태에서, 폴리뉴클레오티드는 폴리펩티드를 발현할 수 있는 재조합 폴리뉴클레오티드를 생성시키도록 유전자 발현을 제어하는 하나 이상의 이종성 조절 또는 제어 서열에 작동가능하게 연결된다. 일부 실시양태에서, 변이체 PGA 아실라제를 코딩하는 이종성 폴리뉴

클레오티드를 함유하는 발현 구성물은 적절한 숙주 세포 내로 도입되어 변이체 PGA 아실라제를 발현한다.

[0136] 당업계의 숙련가는 유전자 코드의 축퇴성에 기인하여, 본 발명의 변이체 PGA 아실라제 폴리펩티드를 코딩하는 다수의 뉴클레오티드 서열이 존재함을 이해한다. 예를 들어, 코돈 AGA, AGG, CGA, CGC, CGG, 및 CGU는 모두 아미노산 아르기닌을 코딩한다. 따라서, 아르기닌이 코돈에 의해 특정되는 본 발명의 핵산 내 모든 위치에서, 코돈은 코딩된 폴리펩티드를 변경시키지 않고 상기 기술된 상응하는 코돈 중 임의의 것으로 변경될 수 있다. RNA 서열의 "U"는 DNA 서열의 "T"에 상응함을 이해한다. 본 발명은 가능한 코돈 선택을 기반으로 조합을 선택하여 제조될 수 있는 본 발명의 폴리펩티드를 코딩하는 핵산 서열의 각각의 모든 가능한 변이를 고려하고, 제공한다.

[0137] 상기에 나타낸 바와 같이, PGA를 코딩하는 DNA 서열은 또한 높은 코돈 용법 편향 코돈(동일한 아미노산을 코딩하는 다른 코돈보다 단백질 코딩 영역에서 더 높은 빈도로 사용되는 코돈)에 대해 디자인될 수도 있다. 바람직한 코돈은 단일 유전자에서 코돈 용법, 공통 기능 또는 기원의 유전자 세트, 고도로 발현되는 유전자, 전체 유기체의 집합 단백질 코딩 영역 내 코돈 빈도, 관련 유기체의 집합 단백질 코딩 영역 내 코돈 빈도, 또는 그의 조합과 관련하여 결정될 수 있다. 그 빈도가 유전자 발현도에 따라 증가하는 코돈은 전형적으로 발현에 최적인 코돈이다. 특히, DNA 서열은 특정 숙주 유기체에서의 발현을 위해 최적화될 수 있다. 다변량 분석(예컨대, 군집 분석 또는 대응 분석을 사용) 및 유전자에 사용되는 코돈의 유효수를 비롯한, 특정 유기체에서 코돈 빈도(예컨대, 코돈 용법, 상대 동의 코돈 용법) 및 코돈 선호도를 결정하는 다양한 방법이 당업계에 널리 공지되어 있다. 코돈 용법을 수득하기 위한 데이터 공급원은 단백질을 코딩할 수 있는 임의의 이용가능한 뉴클레오티드 서열에 의존할 수 있다. 이들 데이터 세트는 발현되는 단백질을 코딩하는 것으로 실제로 알려진 핵산 서열(예컨대, 완전한 단백질 코딩 서열-CDS), 발현된 서열 태그(ESTS), 또는 게놈 서열의 예상되는 코딩 영역을 포함한다. 변이체 PGA를 코딩하는 폴리뉴클레오티드는 당업계에 공지된 임의의 적합한 방법을 사용해 제조될 수 있다. 전형적으로, 올리고뉴클레오티드는 개별적으로 합성된 후, (예컨대, 효소적 또는 화학적 라이게이션 방법, 또는 폴리머라제 매개 방법에 의해) 연결되어 본질적으로 임의의 바람직한 연속되는 서열을 형성한다. 일부 실시양태에서, 본 발명의 폴리뉴클레오티드는 자동화 합성 방법을 포함하나, 이에 제한되지 않는, 당업계에 공지된 임의의 적합한 방법을 사용하여 화학적 합성에 의해 제조된다. 예를 들어, 포스포르아미다이트 방법에서, 올리고뉴클레오티드가 합성되고(자동화 DNA 합성기에서), 정제, 어닐링, 라이게이션되고, 적절한 벡터에 클로닝된다. 일부 실시양태에서, 이중 가닥 DNA 단편은 상보성 가닥을 합성하고, 적절한 조건하에서 함께 가닥들을 어닐링하거나, 또는 적절한 프라이머 서열과 함께 DNA 폴리머라제를 사용하여 상보성 가닥을 부가하여 수득된다. 본 발명에서 유용한 방법을 제공하는 수많은 일반 및 표준 교재가 당업자에게 널리 공지되어 있다.

[0138] 조작된 PGA는 상기 논의된 바와 같이, 돌연변이유발법 및/또는 유도 진화 방법을 자연적으로 발생된 PGA를 코딩하는 폴리뉴클레오티드에 수행함으로써 수득될 수 있다. 돌연변이유발법은 무작위 및 부위 지정 돌연변이유발법을 비롯한, 당업계에 공지된 기술 중 임의의 것에 따라 수행될 수 있다. 유도 진화는 셔플링을 비롯한, 개선된 변이체에 대해 스크리닝하는 당업계에 공지된 기술 중 임의의 것으로 수행될 수 있다. 사용되는 다른 유도 진화 방법으로는 스태거드 확장 프로세스(StEP: staggered extension process), 시험관내 재조합법, 돌연변이성 PCR, 카세트 돌연변이유발법, 중첩 연장에 의한 스플라이싱(SOEing: splicing by overlap extension), ProSAR™ 유도 진화 방법 등 뿐만 아니라, 임의의 다른 적합한 방법을 포함하나, 이에 제한되지 않는다.

[0139] 돌연변이유발 처리 후 수득된 클론은 원하는 개선된 효소 특성을 가지는 조작된 PGA에 대해 스크리닝된다. 발현 라이브러리로부터의 효소 활성 측정은 생성물 형성 속도를 모니터링하는 표준 생화학 기술을 사용하여 수행될 수 있다. 원하는 개선된 효소 특성이 열 안정성인 경우, 효소 활성은 효소 제제를 정의된 온도에 가하고, 열처리 후 남은 효소 활성의 양을 측정한 후에 측정될 수 있다. 이어서, PGA를 코딩하는 폴리뉴클레오티드를 함유하는 클론을 단리시키고, 서열분석하여 (있다면) 뉴클레오티드 서열 변이를 확인하고, 숙주 세포에서 효소를 발현시키는 데 사용한다.

[0140] 조작된 폴리펩티드의 서열이 공지되어 있는 경우, 효소를 코딩하는 폴리뉴클레오티드는 공지된 합성 방법에 따라, 표준 고체상 방법으로 제조될 수 있다. 일부 실시양태에서, 최대 약 100개 염기로 이루어진 단편은 개별적으로 합성된 후, (예컨대, 효소적 또는 화학적 라이게이션 방법, 또는 폴리머라제 매개 방법에 의해) 연결되어 임의의 원하는 연속되는 서열을 형성할 수 있다. 예를 들어, 본 발명의 폴리뉴클레오티드 및 올리고뉴클레오티드는 (예컨대, 전형적으로 자동화 합성 방법에서 실시되는 바와 같이, 문헌 [Beaucage et al., Tet. Lett., 22:1859-69 [1981]]에 기술된 고전적 포스포르아미다이트 방법, 또는 [Matthes et al., EMBO J., 3:801-05 [1984]]에 기술된 방법을 사용하여) 화학 합성에 의해 제조될 수 있다. 포스포르아미다이트 방법에 따라, 올리고뉴클레오티드가 합성되고(자동화 DNA 합성기에서), 정제, 어닐링, 라이게이션되고, 적절한 벡터에 클로닝된다. 추가로, 본질적으로 임의의 핵산은 임의의 다양한 상업적 공급처에서 수득할 수 있다(예컨대, The

Midland Certified Reagent Company: 미국 텍사스주 미들랜드 소재, The Great American Gene Company: 미국 캘리포니아주 라모나 소재, ExpressGen Inc.: 미국 일리노이주 시카고 소재, Operon Technologies Inc.: 미국 캘리포니아주 앨러미다 소재 및 다수의 다른 공급처).

[0141] 본 발명은 또한 본원에 제공된 바와 같이, 적어도 하나의 변이체 PGA를 코딩하는 서열을 포함하는 재조합 구성물을 제공한다. 일부 실시양태에서, 본 발명은 이종성 프로모터에 작동가능하게 연결된 변이체 PGA 폴리뉴클레오티드를 포함하는 발현 벡터를 제공한다. 일부 실시양태에서, 본 발명의 발현 벡터는 숙주 세포가 변이체 PGA 단백질을 발현할 수 있게 허용하는 적절한 숙주 세포를 형질전환시키는 데 사용된다. 진균 및 다른 유기체에서의 단백질의 재조합 발현을 위한 방법은 당업계에 널리 공지되어 있고, 다수의 발현 벡터가 이용가능하거나, 또는 통상의 방법을 사용하여 구성될 수 있다. 일부 실시양태에서, 본 발명의 핵산 구성물은 본 발명의 핵산 서열이 삽입된, 벡터, 예컨대, 플라스미드, 코스미드, 파지, 바이러스, 박테리아 인공 염색체(BAC: bacterial artificial chromosome), 효소 인공 염색체(YAC: yeast artificial chromosome) 등을 포함한다. 일부 실시양태에서, 본 발명의 폴리뉴클레오티드는 변이체 PGA 폴리펩티드(들)를 발현하는 데 적합한 다양한 발현 벡터 중 어느 하나의 것 도입된다. 적합한 벡터로는 염색체, 비염색체 및 합성 DNA 서열(예컨대, SV40의 유도체) 뿐만 아니라, 박테리아 플라스미드, 파지 DNA, 배큘로바이러스, 효모 플라스미드, 플라스미드와 파지 DNA의 조합으로부터 유도된 벡터, 바이러스 DNA, 예컨대, 백시니아, 아데노바이러스, 계두 바이러스, 가성광견병, 아데노바이러스, 아데노 연관 바이러스, 레트로바이러스, 및 다수의 다른 것들을 포함하나 이에 제한되지 않는다. 세포에 유전 물질을 형질전환시키고, 복제가 바람직하면, 관련 숙주에서 복제가능하고 생존가능한 임의의 적합한 벡터가 본 발명에서 사용된다. 일부 실시양태에서, 구성물은 단백질 코딩 서열에 작동가능하게 연결된 프로모터를 포함하나, 이에 제한되지 않는 조절 서열을 추가로 포함한다. 다수의 적합한 벡터 및 프로모터가 당업자에게 공지되어 있다. 실제로, 일부 실시양태에서, 특정 숙주에서 높은 발현 수준을 수득하기 위해, 종종 이종성 프로모터의 제어하에 본 발명의 변이체 PGA를 발현시키는 것이 유용하다. 일부 실시양태에서, 프로모터 서열은 당업계에 공지된 임의의 적합한 방법을 사용해 변이체 PGA 코딩 서열의 5' 영역에 작동가능하게 연결된다. 변이체 PGA의 발현을 위해 유용한 프로모터의 예로는 진균으로부터의 프로모터를 포함하나, 이에 제한되지 않는다. 일부 실시양태에서, 진균 균주의 PGA 유전자 이외의 유전자의 발현을 구동시키는 프로모터 서열이 사용된다. 비제한적인 예로서, 엔도글루카나제를 코딩하는 유전자로부터의 진균 프로모터가 사용될 수 있다. 일부 실시양태에서, PGA의 유래 기점이 된 진균 균주 이외의 다른 진균 균주에서의 PGA 유전자 발현을 구동시키는 프로모터 서열이 사용된다. 섬유상 진균 숙주 세포에서 본 발명의 뉴클레오티드 구성물의 전사를 지시하는 데 유용한 다른 적합한 프로모터의 예로는 아스퍼질러스 오리재 TAKA 아밀라제, 리조무코르 미에헤이 아스파르트산 프로테이나제, 아스퍼질러스 니거 중성 알파 아밀라제, 아스퍼질러스 니거 산 안정 알파 아밀라제, 아스퍼질러스 니거 또는 아스퍼닐러스 아와모리(*Aspergillus awamori*) 글루코아밀라제(glaA), 리조무코르 미에헤이 리파제, 아스퍼질러스 오리재 알칼리성 프로테아제, 아스퍼질러스 오리재 트리오스 포스페이트 이소머라제, 아스퍼질러스 니둘란스(*Aspergillus nidulans*) 아세트아미다제, 및 푸사리움 옥시스포럼(*Fusarium oxysporum*) 트립신 유사 프로테아제(예컨대, WO 96/00787(본원에서 참조로 포함된다) 참조)에 대한 유전자로부터 수득된 프로모터 뿐만 아니라, NA2-tpi 프로모터(아스퍼질러스 니거 중성 알파 아밀라제 및 아스퍼질러스 오리재 트리오스 포스페이트 이소머라제에 대한 유전자 유래의 프로모터의 하이브리드), 프로모터, 예컨대, *cbh*1, *cbh*2, *egl*1, *egl*2, *pep*A, *hfb*1, *hfb*2, *xyn*1, *amy*, 및 *gla*A(예컨대, 문헌 [Nunberg *et al.*, Mol. Cell Biol., 4:2306 -2315 [1984]]; [Boel *et al.*, EMBO J., 3:1581-85 [1984]]; 및 유럽 특허 출원 137280(상기 문헌 모두 본원에서 참조로 포함된다), 및 그의 돌연변이체, 말단절단형, 및 하이브리드 프로모터를 포함하나, 이에 제한되지 않는다.

[0142] 효모 숙주 세포에서, 유용한 프로모터로는 사카로마이세스 세레비지아에 에놀라제(*eno-1*), 사카로마이세스 세레비지아에 갈락토키나제(*gal1*), 사카로마이세스 세레비지아에 알콜 데히드로게나제/글리세르알데히드-3-포스페이트 데히드로게나제(*ADH2/GAP*), 및 S. 세레비지아에(*S. cerevisiae*) 3-포스포글리세레이트 키나제에 대한 유전자로부터의 것을 포함하나, 이에 제한되지 않는다. 효모 숙주 세포에 유용한 추가의 유용한 프로모터는 당업계에 공지되어 있다(예컨대, 문헌 [Romanos *et al.*, Yeast 8:423-488 [1992]](본원에서 참조로 포함된다) 참조). 추가로, 진균에서의 키티나제 생산과 연관된 프로모터가 본 발명에서 사용된다(예컨대, 문헌 [Blaiseau and Lafay, Gene 120243-248 [1992]]; [Limon *et al.*, Curr. Genet., 28:478-83 [1995]](상기 두 문헌 모두 본원에서 참조로 포함된다) 참조).

[0143] 박테리아 숙주 세포의 경우, 본 개시내용의 핵산 구성물의 전사를 지시하는 데 적합한 프로모터로는 이. 콜라이 lac 오페론, 이. 콜라이 trp 오페론, 박테리오파지 λ, 스트렙토마이세스 코엘리컬러(*Streptomyces coelicolor*) 아가라제 유전자(dagA), 바실러스 섭틸리스 레반수크라제 유전자(sacB), 바실러스 리체니포르미스 알파 아밀라제 유전자(amyL), 바실러스 스테아로써모필러스 말토스형성 아밀라제 유전자(amyM), 바실러스 아밀로리케파시엔

스(*Bacillus amyloliquefaciens*) 알파 아밀라제 유전자(amyQ), 바실러스 리체니포르미스 페니실리나제 유전자(penP), 바실러스 섭틸리스 xylA 및 xylB 유전자, 및 원핵생물 베타 락타마제 유전자로부터 수득된 프로모터(예컨대 문헌 [Villa-Kamaroff et al., Proc. Natl. Acad. Sci. USA 75: 3727-3731 [1978]] 참조) 뿐만 아니라, tac 프로모터(예컨대 문헌 [DeBoer et al., Proc. Natl. Acad. Sci. USA 80: 21-25 [1983]] 참조)를 포함하나, 이에 제한되지 않는다.

[0144] 일부 실시양태에서, 본 발명의 클로닝된 변이체 PGA는 또한 전사를 종결하기 위해 숙주 세포에 의해 인식되는 서열인, 적합한 전사 종결인자 서열을 가진다. 종결인자 서열은 폴리펩티드를 코딩하는 핵산 서열의 3' 말단에 작동가능하게 연결된다. 선택된 숙주 세포에서 기능성인 임의의 종결인자가 본 발명에서 사용된다. 섬유상 진균 숙주 세포에 대한 예시적인 전사 종결인자로는 아스퍼질러스 오리재 TAKA 아밀라제, 아스퍼질러스 니거 글루코아밀라제, 아스퍼질러스 니둘란스 안트라닐레이트 시타제, 아스퍼질러스 니거 알파 글루코시다제, 및 푸사리움 옥시스포럼 트립신 유사 프로테아제에 대한 유전자로부터 수득된 것을 포함하나, 이에 제한되지 않는다(또한, 미국 특허 번호 7,399,627(본원에서 참조로 포함된다) 참조). 일부 실시양태에서, 효모 숙주 세포에 대한 예시적인 종결인자로는 사카로마이세스 세레비지아에 에놀라제, 사카로마이세스 세레비지아에 시토크롬 C(CYC1), 및 사카로마이세스 세레비지아에 글리세르알데히드-3-포스페이트 데히드로게나제에 대한 유전자로부터 수득된 것들을 포함한다. 효모 숙주 세포에 대한 다른 유용한 종결인자는 당업자에게 널리 공지되어 있다(예컨대, 문헌 [Romanos *et al.*, Yeast 8:423-88 [1992]] 참조).

[0145] 일부 실시양태에서, 적합한 리더 서열은 숙주 세포에 의한 번역에 중요한 mRNA의 비번역 영역인, 클로닝된 변이체 PGA 서열의 일부이다. 리더 서열은 폴리펩티드를 코딩하는 핵산 서열의 5' 말단에 작동가능하게 연결된다. 선택된 숙주 세포에서 기능성인 임의의 리더 서열이 본 발명에서 사용된다. 섬유상 진균 숙주 세포에 대한 예시적인 리더로는 아스퍼질러스 오리재 TAKA 아밀라제 및 아스퍼질러스 니둘란스 트리오스 포스페이트 이소머라제에 대한 유전자로부터 수득된 것들을 포함하나, 이에 제한되지 않는다. 효모 숙주 세포에 대해 적합한 리더로는 사카로마이세스 세레비지아에 에놀라제(ENO-1), 사카로마이세스 세레비지아에 3-포스포글리세레이트 키나제, 사카로마이세스 세레비지아에 알파 인자, 및 사카로마이세스 세레비지아에 알콜 데히드로게나제/글리세르알데히드-3-포스페이트 데히드로게나제(ADH2/GAP)에 대한 유전자로부터 수득된 것들을 포함하나, 이에 제한되지 않는다.

[0146] 일부 실시양태에서, 본 발명의 서열은 또한 핵산 서열의 3' 말단에 작동가능하게 연결된 서열이고, 전사시, 전사된 mRNA에 폴리아데노신 잔기를 부가하는 신호로서 숙주 세포에 의해 인식되는, 폴리아데닐화 서열을 포함한다. 선택된 숙주 세포에서 기능성인 임의의 폴리아데닐화 서열이 본 발명에서 사용된다. 섬유상 진균 숙주 세포에 대한 예시적인 폴리아데닐화 서열로는 아스퍼질러스 오리재 TAKA 아밀라제, 아스퍼질러스 니거 글루코아밀라제, 아스퍼질러스 니둘란스 안트라닐레이트 시타제, 푸사리움 옥시스포럼 트립신 유사 프로테아제, 및 아스퍼질러스 니거 알파 글루코시다제에 대한 유전자로부터 수득된 것들을 포함하나, 이에 제한되지 않는다. 효모 숙주 세포에 대한 유용한 폴리아데닐화 서열은 당업계에 공지되어 있다(예컨대, 문헌 [Guo and Sherman, Mol. Cell. Biol., 15:5983-5990 [1995]] 참조).

[0147] 일부 실시양태에서, 제어 서열은 폴리펩티드의 아미노 말단에 연결된 아미노산 서열을 코딩하는 신호 펩티드 코딩 영역을 포함하고, 코딩된 폴리펩티드를 세포의 분비 경로로 유도한다. 핵산 서열의 코딩 서열의 5' 단부는 본질적으로, 분비되는 폴리펩티드를 코딩하는 코딩 영역의 세그먼트와 함께 번역 리딩 프레임내에서 자연적으로 연결된 신호 펩티드 코딩 영역을 함유할 수 있다. 대안적으로, 코딩 서열의 5' 단부는 코딩 서열에 외래적인 신호 펩티드 코딩 영역을 함유할 수 있다. 외래 신호 펩티드 코딩 영역은 코딩 서열이 자연적으로 신호 펩티드 코딩 영역을 함유하지 않는 경우에 요구될 수 있다.

[0148] 대안적으로, 외래 신호 펩티드 코딩 영역은 폴리펩티드의 분비를 강화시키기 위해 천연 신호 펩티드 코딩 영역을 단순히 교체할 수 있다. 그러나, 발현된 폴리펩티드를 선택된 숙주 세포의 분비 경로로 유도하는 임의의 신호 펩티드 코딩 영역이 본 발명에 사용될 수 있다.

[0149] 박테리아 숙주 세포에 대해 효과적인 신호 펩티드 코딩 영역으로는 바실러스 NCIB 11837 말토스형성 아밀라제, 바실러스 스테아로써모필러스 알파 아밀라제, 바실러스 리체니포르미스 섭틸리신, 바실러스 리체니포르미스 베타 락타마제, 바실러스 스테아로써모필러스 중성 프로테아제(nprT, nprS, nprM), 및 바실러스 섭틸리스 prsA에 대한 유전자로부터 수득된 신호 펩티드 코딩 영역을 포함하나, 이에 제한되지 않는다. 추가의 신호 펩티드는 당업계에 공지되어 있다(예컨대, 문헌 [Simonen and Palva, Microbiol. Rev., 57: 109-137 [1993]] 참조).

[0150] 섬유상 진균 숙주 세포에 대해 효과적인 신호 펩티드 코딩 영역으로는 아스퍼질러스 오리재 TAKA 아밀라제, 아스퍼질러스 니거 중성 아밀라제, 아스퍼질러스 니거 글루코아밀라제, 리조무코르 미에헤이 아스파르트산 프로테

이나제, 휴미콜라 인솔렌스 셀룰라제, 및 휴미콜라 라누기노사 리파제에 대한 유전자로부터 수득된 신호 펩티드 코딩 영역을 포함하나, 이에 제한되지 않는다.

[0151] 효모 숙주 세포에 유용한 신호 펩티드는 사카로마이세스 세레비지아에 알파 인자 및 사카로마이세스 세레비지아에 인버타제에 대한 유전자를 포함하나, 이에 제한되지 않는다. 다른 유용한 신호 펩티드 코딩 영역은 당업계에 공지되어 있다(예컨대, 문헌 [Romanos et al., [1992], 상기 문헌 동일] 참조).

[0152] 일부 실시양태에서, 제어 서열은 폴리펩티드의 아미노 말단에 위치하는 아미노산 서열을 코딩하는 프로펩티드 코딩 영역을 포함한다. 생성된 폴리펩티드는 프로효소 또는 프로폴리펩티드(또는 일부 경우에서 자이모겐)로 알려져 있다. 프로폴리펩티드는 일반적으로 불활성이고, 프로폴리펩티드로부터 프로펩티드의 촉매성 또는 자가촉매성 절단에 의해 성숙한 활성 PGA 폴리펩티드로 전환될 수 있다. 프로펩티드 코딩 영역은 바실러스 섭틸리스 알칼리성 프로테아제(aprE), 바실러스 섭틸리스 중성 프로테아제(nprT), 사카로마이세스 세레비지아에 알파 인자, 리조무코르 미에헤이 아스파르트산 프로테이나제, 및 마이셀리오프토라 써모필라(*Myceliophthora thermophila*) 락타제에 대한 유전자로부터 수득될 수 있다(예컨대, WO 95/33836 참조).

[0153] 신호 펩티드 및 프로펩티드 영역, 둘 모두가 폴리펩티드의 아미노 말단에 존재하는 경우, 프로펩티드 영역은 폴리펩티드의 아미노 말단 다음에 위치하고, 신호 펩티드 영역은 프로펩티드 영역의 아미노 말단 다음에 위치한다.

[0154] 일부 실시양태에서, 조절 서열은 또한 숙주 세포의 성장 대비 폴리펩티드의 발현이 조절될 수 있도록 하기 위해 사용된다. 조절 시스템의 예는 조절 화합물의 존재를 비롯한, 화학적 또는 물리적 자극에 대응하여 유전자의 발현을 작동시키거나, 또는 작동시키지 않는 것이다. 원핵생물 숙주 세포에서, 적합한 조절 서열로는 lac, tac, 및 trp 오퍼레이터 시스템을 포함하나, 이에 제한되지 않는다. 효모 숙주 세포에서, 적합한 조절 시스템은 예로서, ADH2 시스템 또는 GAL1 시스템을 포함한다. 섬유상 진균에서, 적합한 조절 서열은 AKA 알파 아밀라제 프로모터, 아스퍼질러스 니거 글루코아밀라제 프로모터, 및 아스퍼질러스 오리재 글루코아밀라제 프로모터를 포함한다.

[0155] 조절 서열의 다른 예는 유전자 증폭을 가능하게 하는 것들이다. 진핵생물 시스템에서, 이들은 메토트렉세이트의 존재에서 증폭되는, 디히드로폴레이트 리덕타제 유전자, 및 중금속으로 증폭되는, 메탈로티오네인 유전자를 포함한다. 이러한 경우에서, 본 발명의 PGA 폴리펩티드를 코딩하는 핵산 서열은 조절 서열과 함께 작동가능하게 연결될 것이다.

[0156] 따라서, 추가 실시양태에서, 본 발명은 조작된 PGA 폴리펩티드 또는 그의 변이체를 코딩하는 폴리뉴클레오티드, 및 그들이 도입되는 숙주의 유형에 따라서, 하나 이상의 발현 조절 영역, 예컨대, 프로모터 및 종결인자, 복제 기점 등을 포함하는 재조합 발현 벡터를 제공한다. 일부 실시양태에서, 상기 기술된 다양한 핵산 및 제어 서열은 함께 연결되어 하나 이상의 편리한 제한효소 부위를 포함하여 그 부위에서 폴리펩티드를 코딩하는 핵산 서열의 삽입 또는 치환을 가능하게 할 수 있는 재조합 발현 벡터가 생성된다. 대안적으로, 일부 실시양태에서, 핵산 서열은 발현을 위해 적절한 벡터에 핵산 서열 또는 서열을 포함하는 핵산 구성물을 삽입시켜 발현된다. 발현 벡터 생성시, 코딩 서열은 상기 코딩 서열이 발현을 위해 적절한 제어 서열과 작동가능하게 연결되도록 벡터에 위치한다.

[0157] 재조합 발현 벡터는 편리하게 재조합 DNA 방법에 따라 수행될 수 있고, 폴리뉴클레오티드 서열을 발현시킬 수 있는, 임의의 적합한 벡터(예컨대, 플라스미드 또는 바이러스)를 포함한다. 벡터의 선택은 전형적으로 벡터가 도입되는 숙주 세포와 벡터의 상용성에 의존한다. 일부 실시양태에서, 벡터는 선형이거나, 또는 폐쇄된 고리형 플라스미드이다.

[0158] 일부 실시양태에서, 발현 벡터는 자가 복제 벡터(즉, 염색체외 엔티티로서 존재하고, 그 복제가 염색체 복제와는 독립적인 벡터, 예컨대, 플라스미드, 염색체외 요소, 미니염색체 또는 인공 염색체)이다. 일부 실시양태에서, 벡터는 자가 복제를 보장하는 임의 수단을 함유한다. 대안적으로, 일부 다른 실시양태에서, 숙주 세포 내로의 도입시, 벡터는 게놈 내로 통합되고, 그가 내부에 통합되어 염색체(들)와 함께 복제된다. 추가로, 추가 실시양태에서, 단일 벡터 또는 플라스미드 또는 숙주 세포의 게놈에 도입되는 전체 DNA를 함께 함유하는 2개 이상의 벡터 또는 플라스미드, 또는 트랜스포존이 사용된다.

[0159] 일부 실시양태에서, 본 발명의 발현 벡터는 형질전환된 세포의 용이한 선별을 가능하게 하는, 하나 이상의 선별 가능한 마커를 함유한다. "선별가능한 마커"는 그의 생성물이 살생물성 또는 바이러스 내성, 항미생물제 또는 중금속에 대한 내성, 영양요구성에 대해 자가영양성을 제공하는 유전자이다. amdS(아세트아미다제), argB(오르

니틴 카바모일트랜스퍼라제), bar(포스피노트리신 아세틸트랜스퍼라제), hph(히그로마이신 포스포트랜스퍼라제), niaD(니트레이트 리덕타제), pyrG(오로티딘-5'-포스페이트 데카복실라제), sC(술페이트 아데닐트랜스퍼라제), 및 trpC(안트라닐레이트 시타제) 뿐만 아니라, 그의 등가물을 포함하나, 이에 제한되지 않는, 섬유상 진균 숙주 세포에 사용하기 적합한 임의의 선별가능한 마커가 본 발명에서 사용된다. 예컨대, 아스퍼질러스와 같은 숙주 세포에서 유용한 추가의 마커로는 아스퍼질러스 니둘란스 또는 아스퍼질러스 오리재의 amdS 및 pyrG 유전자, 및 스트렙토마이세스 히그로스코피커스(*Streptomyces hygroscopicus*)의 bar 유전자를 포함하나, 이에 제한되지 않는다. 효모 숙주 세포에 적합한 마커로는 ADE2, HIS3, LEU2, LYS2, MET3, TRP1, 및 URA3을 포함하나, 이에 제한되지 않는다. 박테리아 선별가능한 마커의 예로는 바실러스 섭틸리스 또는 바실러스 리체니포르미스로부터의 *dal* 유전자, 또는 항생제 내성, 예컨대, 암피실린, 카나마이신, 클로람페니콜, 및 또는 테트라사이클린 내성을 부여하는 마커를 포함하나, 이에 제한되지 않는다.

[0160] 일부 실시양태에서, 본 발명의 발현 벡터는 숙주 세포의 게놈 내로의 벡터의 통합 또는 게놈과 독립적으로 세포 내에서 벡터의 자가 복제를 가능하게 하는 성분(들)을 함유한다. 숙주 세포 게놈에의 통합을 포함하는 일부 실시양태에서, 벡터는 폴리펩티드를 코딩하는 핵산 서열 또는 상동성 또는 비상동성 재조합에 의해 게놈 내로의 벡터의 통합을 위한 벡터의 임의의 다른 성분에 의존한다.

[0161] 일부 대안적인 실시양태에서, 발현 벡터는 상동성 재조합에 의한 숙주 세포의 게놈 내로의 통합을 지시하기 위한 추가의 핵산 서열을 함유한다. 추가의 핵산 서열을 통해 벡터는 염색체(들) 내 정확한 위치(들)에서 숙주 세포 게놈 내로 통합될 수 있다. 정확한 위치에 통합될 수 있는 가능성을 증가시키기 위해, 통합 요소는 바람직하게 상동성 재조합의 확률을 증가시키기 위해 상응하는 표적 서열과 고도의 상동성인, 충분한 개수의 뉴클레오티드, 예컨대, 100 내지 10,000개의 염기쌍, 바람직하게, 400 내지 10,000개의 염기쌍, 가장 바람직하게 800 내지 10,000개의 염기쌍을 함유한다. 통합 요소는 숙주 세포의 게놈 내 표적 서열과 상동성인 임의 서열일 수 있다. 추가로, 통합 요소는 비코딩 또는 코딩 핵산 서열일 수 있다. 한편, 벡터는 비상동성 재조합에 의해 숙주 세포의 게놈 내로 통합될 수 있다.

[0162] 자가 복제를 위해, 벡터는 해당 숙주 세포에서 벡터가 자가 복제할 수 있도록 하는 복제 기점을 추가로 포함할 수 있다. 박테리아 복제 기점의 예로는 P15A ori 또는 이. 콜라이에서 복제할 수 있게 하는 플라스미드 pBR322, pUC19, pACYC177(이 플라스미드는 P15A ori를 가진다), 또는 pACYC184, 및 바실러스에서 복제할 수 있게 하는 pUB110, pE194, pTA1060, 또는 pAMβ1의 복제 기점이 있다. 효모 숙주 세포에서 사용하기 위한 복제 기점의 예로는 2 미크론 복제 기점, ARS1, ARS4, ARS1 및 CEN3의 조합, 및 ARS4 및 CEN6의 조합이 있다. 복제 기점은 숙주 세포에서 그의 기능성을 온도 감수성으로 만드는 돌연변이를 가지는 것일 수 있다(예컨대, 문헌 [Ehrlich, Proc. Natl. Acad. Sci. USA 75:1433 [1978]] 참조).

[0163] 일부 실시양태에서, 유전자 생성물의 제조를 증가시키기 위해 본 발명의 핵산 서열의 1개 초과의 카피를 숙주 세포 내로 삽입시킨다. 핵산 서열의 카피 수 증가는 서열의 적어도 하나의 추가 카피를 숙주 세포 게놈 내로 통합시키거나, 또는 선별가능한 마커 유전자의 증폭된 카피와, 그에 따라 핵산 서열의 추가 카피를 함유하는 세포가 적절한 선별제의 존재하에서 세포를 배양하는 것에 의해 선택될 수 있는 핵산 서열과 증폭가능한 선별가능한 마커 유전자를 포함시켜 수득될 수 있다.

[0164] 본 발명에서 사용하기 위한 다수의 발현 벡터는 상업적으로 이용가능하다. 적합한 상업적 발현 벡터로는 포유동물 숙주 세포에서의 발현을 위한 CMV 프로모터 및 hGH 폴리아데닐화 부위 및 이. 콜라이에서의 증폭을 위한 pBR322 복제 기점 및 암피실린 내성 마커를 포함하는, p3xFLAGTM™ 발현 벡터(Sigma-Aldrich Chemicals)를 포함하나, 이에 제한되지 않는다. 다른 적합한 발현 벡터로는 pBluescriptII SK(-) 및 pBK-CMV(Stratagene), 및 pBR322(Gibco BRL), pUC(Gibco BRL), pREP4, pCEP4(Invitrogen) 또는 pPoly(예컨대, 문헌 [Lathe et al., Gene 57:193-201 [1987]] 참조)로부터 유래된 플라스미드를 포함하나, 이에 제한되지 않는다.

[0165] 따라서, 일부 실시양태에서, 적어도 하나의 변이체 PGA를 코딩하는 서열을 포함하는 벡터는 벡터의 증식 및 변이체 PGA(들)의 발현을 가능하게 하기 위해 숙주 세포로 형질전환된다. 일부 실시양태에서, 변이체 PGA는 신호 펩티드를 제거하도록 번역 후 변형되고, 일부 경우에서 분비 후 절단될 수 있다. 일부 실시양태에서, 상기 기술된 형질전환된 숙주 세포는 변이체 PGA(들)의 발현을 가능하게 하는 조건하에 적합한 영양 배지 중에서 배양된다. 최소 배지, 또는 적절한 보충제를 함유하는 복합 배지를 포함하나, 이에 제한되지 않는, 숙주 세포를 배양하는 데 유용한 임의의 적합한 배지가 본 발명에서 사용된다. 일부 실시양태에서, 숙주 세포는 HTP 배지 중에서 성장된다. 적합한 배지는 다양한 상업적 공급처에서 입수할 수 있거나, 또는 (예컨대, 미국 모식균 배양 수집소(American Type Culture Collection)의 카탈로그에의) 공개된 제조법에 따라 제조될 수 있다.

[0166] 또 다른 측면에서, 본 발명은 본원에 제공된 개선된 PGA 폴리펩티드를 코딩하는 폴리뉴클레오티드를 포함하는 숙주 세포로서, 여기서, 폴리뉴클레오티드는 숙주 세포에서 PGA 효소의 발현을 위해 하나 이상의 제어 서열에 작동적으로 연결되어 있는 것인 숙주 세포를 제공한다. 본 발명의 발현 벡터에 의해 코딩되는 PGA 폴리펩티드를 발현하는 데 사용하기 위한 숙주 세포는 당업계에 널리 공지되어 있고, 박테리아 세포, 예컨대, 이. 콜라이, 바실러스 메가테리움(*Bacillus megaterium*), 락토바실러스 케피르(*Lactobacillus kefir*), 스트렙토마이세스(*Streptomyces*) 및 살모넬라 티피뮤리움(*Salmonella typhimurium*) 세포; 진균 세포, 예컨대, 효모 세포(예컨대, 사카로마이세스 세레비지아에 또는 피치아 파스토리스(*Pichia pastoris*)(ATCC 수탁 번호 201178)); 곤충 세포, 예컨대, 드로소필라(Drosophila) S2 및 스포돕테라(Spodoptera) Sf9 세포; 동물 세포, 예컨대, CHO, COS, BHK, 293, 및 보우스 흑색종 세포; 및 식물 세포를 포함하나, 이에 제한되지 않는다. 상기 기술된 숙주 세포에 적절한 배양 배지 및 성장 조건은 당업계에 널리 공지되어 있다.

[0167] PGA의 발현을 위한 폴리뉴클레오티드는 당업계에 공지된 다양한 방법에 의해 세포 내로 도입될 수 있다. 기술로는 특히 전기천공, 바이오리스틱스 입자 충격, 리포솜 매개 형질감염, 염화칼슘 형질감염, 원형질체 융합을 포함한다. 세포에 폴리뉴클레오티드를 도입시키기 위한 다양한 방법이 당업자에게 공지되어 있다.

[0168] 일부 실시양태에서, 숙주 세포는 진핵생물 세포이다. 적합한 진핵생물 숙주 세포로는 진균 세포, 조류 세포, 곤충 세포, 및 식물 세포를 포함하나, 이에 제한되지 않는다. 적합한 진균 숙주 세포로는 아스코마이코타(*Ascomycota*), 바시디오마이코타(*Basidiomycota*), 듀테로마이코타(*Deuteromycota*), 자이고마이코타(*Zygomycota*), 불완전 진균류를 포함하나, 이에 제한되지 않는다.. 일부 실시양태에서, 진균 숙주 세포는 효모 세포 및 섬유상 진균 세포이다. 본 발명의 섬유상 진균 숙주 세포는 유마이코티나(*Eumycotina*) 아문 및 우마이코타(*Oomycota*) 아문의 모든 섬유상 형태를 포함한다. 섬유상 진균은 키틴, 셀룰로스 및 다른 복합 다당류로 구성된 세포벽을 가지는 영양 균사체를 특징으로 한다. 본 발명의 섬유상 진균 숙주 세포는 효모와 형태학적으로 구별된다.

[0169] 본 발명의 일부 실시양태에서, 섬유상 진균 숙주 세포는 아클리아(*Achlya*), 아크레모니움(*Acremonium*), 아스퍼질러스, 아우레오바시디움(*Aureobasidium*), 비제르칸데라(*Bjerkandera*), 세리포리옵시스(*Ceriporiopsis*), 세팔로스포리움(*Cephalosporium*), 크리소스포리움(*Chrysosporium*), 코클리오보러스(*Cochliobolus*), 코리나스커스(*Corynascus*), 크리포넥트리아(*Cryphonectria*), 크립토코커스(*Cryptococcus*), 코프리너스(*Coprinus*), 코리오러스(*Coriolus*), 디플로디아(*Diplodia*), 엔도티스(*Endothis*), 푸사리움(*Fusarium*), 지베렐라(*Gibberella*), 글리오클라디움(*Gliocladium*), 휴미콜라(*Humicola*), 히포크레아(*Hypocrea*), 마이셀리오프토라(*Myceliophthora*), 무코르(*Mucor*), 뉴로스포라(*Neurospora*), 페니실리움(*Penicillium*), 포도스포라(*Podospora*), 플레비아(*Phlebia*), 피로마이세스(*Piromyces*), 피리쿨라리아(*Pyricularia*), 리조무코르(*Rhizomucor*), 리조퍼스(*Rhizopus*), 스키조필럼(*Schizophyllum*), 스시탈리디움(*Scytalidium*), 스포로트리컴(*Sporotrichum*), 탈라로마이세스(*Talaromyces*), 써모아스커스(*Thermoascus*), 티에라비아(*Thielavia*), 트라메테스(*Trametes*), 톨리포클라디움(*Tolypocladium*), 트리코더마(*Trichoderma*), 베르티실리움(*Verticillium*), 및/또는 볼바리엘라(*Volvariella*), 및/또는 이들의 유성생식형, 또는 무성생식형, 및 이명, 기본명, 또는 분류상 등가물을 포함하나, 이에 제한되지 않는, 임의의 속 및 종의 것이다.

[0170] 본 발명의 일부 실시양태에서, 숙주 세포는 칸디다(*Candida*), 한세눌라(*Hansenula*), 사카로마이세스, 스키조사카로마이세스(*Schizosaccharomyces*), 피치아, 클루이베로마이세스(*Kluyveromyces*), 또는 야로위아(*Yarrowia*) 종의 세포를 포함하나, 이에 제한되지 않는 효모 세포이다. 본 발명의 일부 실시양태에서, 효모 세포는 한세눌라 폴리몰파(*Hansenula polymorpha*), 사카로마이세스 세레비지아에, 사카로마이세스 칼스베르겐시스(*Saccharomyces carlsbergensis*), 사카로마이세스 디아스타티커스(*Saccharomyces diastaticus*), 사카로마이세스 놀벤시스(*Saccharomyces norbensis*), 사카로마이세스 클루이베리(*Saccharomyces kluyveri*), 스키조사카로마이세스 폼베(*Schizosaccharomyces pombe*), 피치아 파스토리스, 피치아 핀란디카(*Pichia finlandica*), 피치아 트레할로필라(*Pichia trehalophila*), 피치아 코다마에(*Pichia kodamae*), 피치아 멤브라내파시엔스(*Pichia membranaefaciens*), 피치아 오푼티아에(*Pichia opuntiae*), 피치아 써모톨레란스(*Pichia thermotolerans*), 피치아 살리크타리아(*Pichia salictaria*), 피치아 케르큄(*Pichia quercuum*), 피치아 피지페리(*Pichia pijperi*), 피치아 스티피티스(*Pichia stipitis*), 피치아 메타놀리카(*Pichia methanolica*), 피치아 안구스타(*Pichia angusta*), 클루이베로마이세스 락티스(*Kluyveromyces lactis*), 칸디다 알비칸스(*Candida albicans*), 또는 야로위아 리포리티카(*Yarrowia lipolytica*)이다.

[0171] 본 발명의 일부 실시양태에서, 숙주 세포는 조류 세포, 예컨대, 클라미도모나스(*Chlamydomonas*)(예컨대, C. 레

인하르드티이(*C. reinhardtii*)) 및 포르미디움(*Phormidium*)(P. sp. ATCC29409)이다.

[0172] 일부 다른 실시양태에서, 숙주 세포는 원핵생물 세포이다. 적합한 원핵생물 세포로는 그람 양성, 그람 음성 및 그람 가변성(Gram-variable) 박테리아 세포를 포함하나, 이에 제한되지 않는다. 아그로박테리움(*Agrobacterium*), 알리사이클로바실러스(*Alicyclobacillus*), 아나바에나(*Anabaena*), 아나시스티스(*Anacystis*), 아시네토박터(*Acinetobacter*), 악시도써머스(*Acidothermus*), 알트로박터(*Arthrobacter*), 아조박터(*Azobacter*), 바실러스, 비피도박테리움(*Bifidobacterium*), 브레비박테리움(*Brevibacterium*), 부티리비브리오(*Butyrivibrio*), 부치네라(*Buchnera*), 캄페스트리스(*Campestris*), 캠플리오박터(*Camplyobacter*), 클로스트리디움(*Clostridium*), 코리네박테리움(*Corynebacterium*), 클로마티움(*Chromatium*), 코프로코커스(*Coprococcus*), 에스케리키아(*Escherichia*), 엔테로코커스(*Enterococcus*), 엔테로박터(*Enterobacter*), 어위니아(*Erwinia*), 푸소박테리움(*Fusobacterium*), 파에칼리박테리움(*Faecalibacterium*), 프란시셀라(*Francisella*), 플라보박테리움(*Flavobacterium*), 지오바실러스(*Geobacillus*), 해모필러스(*Haemophilus*), 헬리코박터(*Helicobacter*), 클렙시엘라(*Klebsiella*), 락토바실러스(*Lactobacillus*), 락토코커스(*Lactococcus*), 일리오박터(*Ilyobacter*), 마이크로코커스(*Micrococcus*), 마이크로박테리움(*Microbacterium*), 메소리조비움(*Mesorhizobium*), 메틸로박테리움(*Methylobacterium*), 메틸로박테리움(*Methylobacterium*), 마이코박테리움(*Mycobacterium*), 나이세리아(*Neisseria*), 판토에아(*Pantoea*), 슈도모나스(*Pseudomonas*), 프로클로로코커스(*Prochlorococcus*), 로도박터(*Rhodobacter*), 로도슈도모나스(*Rhodopseudomonas*), 로도슈도모나스(*Rhodopseudomonas*), 로세버리아(*Roseburia*), 로도스피릴럼(*Rhodospirillum*), 로도코커스(*Rhodococcus*), 세네데스머스(*Scenedesmus*), 스트렙토마이세스, 스트렙토코커스(*Streptococcus*), 시네코커스(*Synecoccus*), 사카로모노스포라(*Saccharomonospora*), 스타필로코커스(*Staphylococcus*), 세라티아(*Serratia*), 살모넬라, 시겔라(*Shigella*), 써모아나에로박테리움(*Thermoanaerobacterium*), 트로페리마(*Tropheryma*), 툴라렌시스(*Tularensis*), 테메쿨라(*Temecula*), 써모시네코코커스(*Thermosynechococcus*), 써모코커스(*Thermococcus*), 우레아플라스마(*Ureaplasma*), 크산토모나스(*Xanthomonas*), 크실렐라(*Xylella*), 여시니아(*Yersinia*) 및 자이모모나스(*Zymomonas*)를 포함하나, 이에 제한되지 않는 임의의 적합한 박테리아 유기체가 본 발명에서 사용된다. 일부 실시양태에서, 숙주 세포는 아그로박테리움, 아시네토박터, 아조박터, 바실러스, 비피도박테리움, 부치네라, 지오바실러스, 캄필로박터, 클로스트리디움, 코리네박테리움, 에스케리키아, 엔테로코커스, 어위니아, 플라보박테리움, 락토바실러스, 락토코커스, 판토에아, 슈도모나스, 스타필로코커스, 살모넬라, 스트렙토코커스, 스트렙토마이세스, 또는 자이모모나스의 종이다. 일부 실시양태에서, 박테리아 숙주 균주는 인간에 비병원성이다. 일부 실시양태에서 박테리아 숙주 균주는 산업용 균주이다. 다수의 박테리아 산업용 균주가 공지되어 있고, 본 발명에 적합하다. 본 발명의 일부 실시양태에서, 박테리아 숙주 세포는 아그로박테리움 종(예컨대, A. 라디오박터(*A. radiobacter*), A. 리조게네스(*A. rhizogenes*), 및 A. 루비(*A. rubi*))이다. 본 발명의 일부 실시양태에서, 박테리아 숙주 세포는 알트로박터 종(예컨대, A. 아우레센스(*A. aurescens*), A. 시트레우스(*A. citreus*), A. 글로비포르미스(*A. globiformis*), A. 히드로카르보글루타미커스(*A. hydrocarboglutamicus*), A. 미소렌스(*A. mysorens*), A. 니코티아나에(*A. nicotianae*), A. 파라피네우스(*A. paraffineus*), A. 프로토폰니아에(*A. protophonniae*), A. 로세오파르크피너스(*A. roseoparqffinus*), A. 술퍼레우스(*A. sulfureus*), 및 A. 우레아파시엔스(*A. ureafaciens*))이다. 본 발명의 일부 실시양태에서, 박테리아 숙주 세포는 바실러스 종(예컨대, B. 투린겐시스(*B. thuringensis*), B. 안트라시스(*B. anthracis*), B. 메가테리움, B. 섭틸리스, B. 렌터스(*B. lentus*), B. 실쿨란스(*B. circulans*), B. 푸밀러스(*B. pumilus*), B. 라우터스(*B. lautus*), B. 코아굴란스(*B. coagulans*), B. 브레비스(*B. brevis*), B. 필머스(*B. firmus*), B. 알카오피우스(*B. alkaophius*), B. 리체니포르미스, B. 클라우시이(*B. clausii*), B. 스테아로써모필러스, B. 할로두란스(*B. halodurans*), 및 B. 아밀로리케파시엔스)이다. 일부 실시양태에서, 숙주 세포는 B. 섭틸리스, B. 푸밀러스, B. 리체니포르미스, B. 메가테리움, B. 클라우시이, B. 스테아로써모필러스, 또는 B. 아밀로리케파시엔스를 포함하나, 이에 제한되지 않는 산업용 바실러스 균주이다. 일부 실시양태에서, 바실러스 숙주 세포는 B. 섭틸리스, B. 리체니포르미스, B. 메가테리움, B. 스테아로써모필러스, 및/또는 B. 아밀로리케파시엔스이다. 일부 실시양태에서, 박테리아 숙주 세포는 클로스트리디움 종(예컨대, C. 아세토부틸리컴(*C. acetobutylicum*), C. 테타니(*C. tetani*) E88, C. 리투세부렌스(*C. lituseburense*), C. 사카로부틸리컴(*C. saccharobutylicum*), C. 펄프린겐스(*C. perfringens*), 및 C. 베이제린키이(*C. beijerinckii*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 코리네박테리움 종(예컨대, C. 글루타미컴(*C. glutamicum*) 및 C. 아세토아시도필럼(*C. acetoacidophilum*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 에스케리키아 종(예컨대, 이. 콜라이)이다. 일부 실시양태에서, 박테리아 숙주 세포는 어위니아 종(예컨대, 예컨대, E. 우레도보라(*E. uredovora*), E. 카로토보라(*E. carotovora*), E. 아나나스(*E. ananas*), E. 헬비콜라(*E. herbicola*), E. 푼타타(*E. punctata*), 및 E. 테레우스(*E. terreus*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 판토에아 종(예컨

대, P. 시트레아(*P. citrea*), 및 P. 아글로메란스(*P. agglomerans*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 슈도모나스 종(예컨대, P. 푸티다(*P. putida*), P. 아에루기노사(*P. aeruginosa*), P. 메발로니이(*P. mevalonii*), 및 *P. sp.* D-01 10)이다. 일부 실시양태에서, 박테리아 숙주 세포는 스트렙토코커스 종(예컨대, S. 에퀴시밀레스(*S. equisimiles*), S. 피오게네스(*S. pyogenes*), 및 S. 우베리스(*S. uberis*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 스트렙토마이세스 종(예컨대, S. 암보파시엔스(*S. ambofaciens*), S. 아크로모게네스(*S. achromogenes*), S. 아벨미틸리스(*S. avermitilis*), S. 코엘리컬러(*S. coelicolor*), S. 아우레오파시엔스(*S. aureofaciens*), S. 아우레우스(*S. aureus*), S. 푼지시디커스(*S. fungicidicus*), S. 그리세우스(*S. griseus*), 및 S. 리비단스(*S. lividans*))이다. 일부 실시양태에서, 박테리아 숙주 세포는 자이모모나스 종(예컨대, 종(예컨대, Z. 모빌리스(*Z. mobilis*), 및 Z. 리포리티카(*Z. lipolytica*))이다.

[0173] 예시적인 숙주 세포는 에스케리키아 콜라이 W3110이다. 발현 벡터는 *lac*I 리프레서의 제어하에 있는 *lac* 프로모터에 작동적으로 연결된 플라스미드 pCK110900에, 개선된 PGA를 코딩하는 폴리뉴클레오티드를 작동적으로 연결시킴으로써 생성하였다. 발현 벡터는 또한 P15a 복제 기점 및 클로람페니콜 내성 유전자를 함유하였다. 에스케리키아 콜라이 W3110에 대상 폴리뉴클레오티드를 함유하는 세포는 상기 세포에 대하여 클로람페니콜 선별을 수행함으로써 단리시켰다.

[0174] 본 발명에서 사용되는 다수의 원핵생물 및 진핵생물 균주는 다수의 배양 수집소, 예컨대, 미국 모식균 배양 수집소(ATCC: American Type Culture Collection), 독일 생물자원센터(DSM: Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH), 사균 배지 중앙 보관소(CBS: Centraalbureau Voor Schimmelcultures) 및 농업 연구소 배양 보관소(Agricultural Research Service Patent Culture Collection), 북방 연구 센터(NRRL: Northern Regional Research Center)를 통해 공중에 의해 용이하게 입수될 수 있다.

[0175] 일부 실시양태에서, 숙주 세포는 단백질 분비, 단백질 안정성 및/또는 단백질의 발현 및/또는 분비에 바람직한 다른 특성을 개선시키는 특징을 가지도록 유전적으로 변형된다. 유전자 변형은 유전자 조작 기술 및/또는 고전적인 미생물학적 기술(예컨대, 화학적 또는 UV 돌연변이유발법 및 후속 선별법)에 의해 달성될 수 있다. 실제로, 일부 실시양태에서, 재조합 변형 및 고전적 선별 기술의 조합을 사용하여 숙주 세포를 제조한다. 재조합 기술을 사용하여, 숙주 세포 내에서 및/또는 배양 배지 중에서 PGA 변이체(들)의 수율을 증가시키는 방식으로 핵산 분자를 도입시키거나, 결실시키거나, 억제시키거나 또는 변형시킬 수 있다. 예를 들어, Alp1 기능의 넉아웃은 프로테아제 결핍된 세포를 초래하고, pyr5 기능의 넉아웃은 피리미딘 결핍 표현형을 가지는 세포를 초래한다. 한 유전자 조작 접근법에서, 상동성 재조합은 코딩된 단백질의 발현을 억제시키기 위하여 생체내에서 유전자를 특이적으로 표적화하여 표적화된 유전자 변형을 유도하는 데 사용된다. 대안적 접근법에서, siRNA, 안티센스 및/또는 리보자임 기술이 유전자 발현을 억제하는 데 사용된다. 세포에서 단백질의 발현을 감소시키기 위한 것으로서, 단백질을 코딩하는 유전자 모두 또는 일부를 결실시키는 것, 및 유전자 생성물의 발현 또는 활성을 파괴시키는 부위 특이적 돌연변이유발법을 포함하나, 이에 제한되지 않는 다양한 방법이 당업계에 공지되어 있다(예컨대, 문헌 [Chaveroche et al., Nucl. Acids Res., 28:22 e97 [2000]]; [Cho et al., Molec. Plant Microbe Interact., 19:7-15 [2006]]; [Maruyama and Kitamoto, Biotechnol Lett., 30:1811-1817 [2008]]; [Takahashi et al., Mol. Gen. Genom., 272: 344-352 [2004]]; 및 [You et al., Arch. Micriobiol.,191:615-622 [2009]](상기 문헌들은 모두 본원에서 참조로 포함된다) 참조). 무작위 돌연변이유발법, 이어서, 바람직한 돌연변이에 스크리닝 또한 사용된다(예컨대, 문헌 [Combier et al., *FEMS Microbiol. Lett.*, **220**:141-8 [2003]]; 및 [Firon et al., *Eukary. Cell* **2**:247-55 [2003]](상기 두 문헌 모두 본원에서 참조로 포함된다) 참조).

[0176] 벡터 또는 DNA 구성물의 숙주 세포 내로의 도입은 인산칼슘 형질감염, DEAE-덱트스란 매개 형질감염, PEG-매개 형질전환, 전기천공, 또는 당업계에 공지된 다른 공통 기술을 포함하나, 이에 제한되지 않는, 당업계에 공지된 임의의 적합한 방법을 사용하여 달성될 수 있다.

[0177] 일부 실시양태에서, 본 발명의 조작된 숙주 세포(즉, "재조합 숙주 세포")는 프로모터를 활성화시키거나, 형질전환체를 선별하거나, 또는 PGA 폴리뉴클레오티드를 증폭시키기에 적절하게 변형된 통상의 영양 배지에서 배양된다. 배양 조건, 예컨대, 온도, pH 등은 발현을 위해 선택된 숙주 세포에 따라 이전에 사용된 것들이고, 당업자에게 널리 공지되어 있다. 언급한 바와 같이, 다수의 표준 참고문헌 및 교재가 박테리아, 식물, 동물(특히, 포유동물) 및 고세균 기원의 세포를 비롯한, 많은 세포의 배양 및 제조를 위해 이용가능하다.

[0178] 일부 실시양태에서, 본 발명의 변이체 PGA 폴리펩티드를 발현하는 세포는 회분식 또는 연속형 발효 조건하에서 성장된다. 고전적인 "회분식 발효"는 폐쇄 시스템으로서, 여기서, 배지의 조성은 발효의 시작시에 설정되어 있

고, 발효 동안 인공적인 변경이 가해지지 않는다. 회분식 시스템의 변형은 본 발명에서 또한 사용되는 "유가식 발효"이다. 상기 변형에서는 발효가 진행됨에 따라 기질이 증분량으로 첨가된다. 유가식 시스템은 이화대사 산물 억제가 아마도 세포의 물질대사를 억제할 수 있는 경우 및 배지 내에 제한된 양의 기질을 가지는 것이 바람직한 경우에 유용하다. 회분식 및 유가식 발효는 당업계에서 일반적이고, 널리 공지되어 있다. "연속 발효"는 정해진 발효 배지가 연속적으로 생물반응기에 첨가되고, 동량의 조건화 배지가 프로세싱 동안 동시에 제거되는 개방형 시스템이다. 연속 발효는 일반적으로 세포를 주로 대수기 성장의 일정한 고밀도로 배양물을 유지시킨다. 연속 발효 시스템은 정상 상태 성장 조건을 유지시키도록 노력한다. 연속 발효 프로세스를 위해 영양분 및 성장 인자를 조정하기 위한 방법 뿐만 아니라, 생성물 형성 속도를 최대화하기 위한 기술이 산업 미생물학 분야에 널리 공지되어 있다.

[0179] 본 발명의 일부 실시양태에서, 무세포 전사/번역 시스템이 변이체 PGA(들)를 제조하는 데 사용된다. 수개의 시스템은 상업적으로 이용가능하고, 방법은 당업자에게 널리 공지되어 있다.

[0180] 본 발명은 변이체 PGA 폴리펩티드, 또는 그의 생물학적 활성 단편을 제조하는 방법을 제공한다. 일부 실시양태에서, 본 방법은 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 1288과 적어도 약 70%(또는 적어도 약 75%, 적어도 약 80%, 적어도 약 85%, 적어도 약 90%, 적어도 약 95%, 적어도 약 96%, 적어도 약 97%, 적어도 약 98%, 또는 적어도 약 99%)의 서열 동일성을 포함하는 아미노산 서열을 코딩하고, 본원에 제공된 바와 같은 적어도 하나의 돌연변이를 포함하는 폴리뉴클레오티드로 형질전환된 숙주 세포를 제공하는 단계; 숙주 세포가 코딩된 변이체 PGA 폴리펩티드를 발현하는 조건하에서 형질전환된 숙주 세포를 배양 배지 중에서 배양하는 단계; 및 임의적으로, 발현된 변이체 PGA 폴리펩티드를 회수 또는 단리시키는 단계, 및/또는 발현된 변이체 PGA 폴리펩티드를 함유하는 배양 배지를 회수 또는 단리시키는 단계를 포함한다. 일부 실시양태에서, 본 방법은 임의적으로 코딩된 PGA 폴리펩티드를 발현시킨 후, 형질전환된 숙주 세포를 용해시키는 단계 및 임의적으로 세포 용해물로부터 발현된 변이체 PGA 폴리펩티드를 회수 및/또는 단리시키는 단계를 추가로 제공한다. 본 발명은 변이체 PGA 폴리펩티드 제조에 적합한 조건하에서 변이체 PGA 폴리펩티드로 형질전환된 숙주 세포를 배양하는 단계 및 변이체 PGA 폴리펩티드를 회수하는 단계를 포함하는, 변이체 PGA 폴리펩티드를 제조하는 방법을 추가로 제공한다. 전형적으로, PGA 폴리펩티드의 회수 또는 단리는 본원에 기술된 것들을 포함하여, 당업계에 널리 공지된 단백질 회수 기술을 사용하여, 숙주 세포 배양 배지, 숙주 세포 또는 그 둘 모두로부터 수행한다. 일부 실시양태에서, 숙주 세포는 원심분리에 의해 수확되고, 물리적 또는 화학적 수단에 의해 파괴되고, 생성된 조 추출물은 추가 정제를 위해 유지된다. 단백질의 발현에 사용된 미생물 세포는 냉동-해동 사이클링, 초음파처리, 기계적 파괴, 및/또는 세포 용해제의 사용을 포함하나, 이에 제한되지 않는 임의의 편리한 방법 뿐만 아니라, 당업자에게 널리 공지된 다수의 다른 적합한 방법에 의해 파괴시킬 수 있다.

[0181] 숙주 세포에서 발현되는 조작된 PGA 효소는 특히, 리소자임 처리, 초음파처리, 여과, 염석, 초원심분리, 및 크로마토그래피를 비롯한, 단백질 정제를 위한 것으로 널리 공지된 기술 중 어느 하나 이상의 것을 사용하여 세포 및/또는 배양 배지로부터 회수될 수 있다. 박테리아, 예컨대, 이. 콜라이로부터 용해 및 단백질의 고효율 추출을 위해 적합한 용액은 상품명 셀라이틱스 B(CelLytic B)™(Sigma-Aldrich)하에 상업적으로 이용가능하다. 따라서, 일부 실시양태에서, 생성된 폴리펩티드는 당업계에 공지된 다수의 방법들 중 임의의 것에 의해 회수/단리되고, 임의적으로, 정제된다. 예를 들어, 일부 실시양태에서, 폴리펩티드는 원심분리, 여과, 추출, 분무 건조, 증발, 크로마토그래피(예컨대, 이온 교환, 친화성, 소수성 상호작용, 크로마토포커싱, 및 크기 배제), 또는 침전을 포함하나, 이에 제한되지 않는 통상의 방법에 의해 영양 배지로부터 단리된다. 일부 실시양태에서, 단백질 리폴딩 단계는 원하는 경우, 성숙한 단백질의 배열 완료시에 사용된다. 추가로, 일부 실시양태에서, 고성능 액체 크로마토그래피(HPLC: high performance liquid chromatography)가 최종 정제 단계에서 사용된다. 예를 들어, 일부 실시양태에서, 당업계에 공지된 방법이 본 발명에서 사용된다(예컨대, 문헌 [Parry et al., Biochem. J., 353:117 [2001]]; 및 [Hong et al., Appl. Microbiol. Biotechnol., 73:1331 [2007]](상기 두 문헌 모두 본원에서 참조로 포함된다) 참조). 실제로, 당업계에 공지된 임의의 적합한 정제 방법이 본 발명에서 사용된다.

[0182] PGA 폴리펩티드의 단리를 위한 크로마토그래피 기술로는 역상 크로마토그래피, 고성능 액상 크로마토그래피, 이온 교환 크로마토그래피, 겔 전기영동, 및 친화성 크로마토그래피를 포함하나, 이에 제한되지 않는다. 특정 효소를 정제하기 위한 조건은 부분적으로는 당업자에게 공지되어 있는 인자들, 예컨대, 순전하, 소수성, 친수성, 분자량, 분자 형상 등에 의존할 것이다.

[0183] 일부 실시양태에서, 친화성 기술이 개선된 PGA 효소를 단리시키는 데 사용된다. 친화성 크로마토그래피 정제를 위해, PGA 폴리펩티드에 특이적으로 결합하는 임의의 항체가 사용될 수 있다. 항체 제조를 위해, 토끼, 마우스, 래트 등을 포함하나, 이에 제한되지 않는 각종 숙주 동물을 PGA의 주사에 의해 면역화시킬 수 있다. PGA 폴리펩

티드를 측쇄 작용기 또는 측쇄 작용기에 부착된 링커에 의해, 적합한 담체, 예컨대, BSA에 부착시킬 수 있다. 프로인트(완전 및 불완전), 미네랄 겔, 예컨대, 수산화알루미늄, 계면 활성 물질, 예컨대, 리소레시틴, 플루로닉 폴리올, 다가 음이온, 펩티드, 오일 에멀션, 키홀 림펫 헤모시아닌, 디니트로페놀, 및 잠재적으로 유용한 인간 애주번트, 예컨대, BCG(바실러스 칼메-구에린: Bacillus Calmette Guerin) 및 코리네박테리움 파르붐(*Corynebacterium parvum*)을 포함하나, 이에 제한되지 않는, 각종의 애주번트가 숙주 종에 따라, 면역학적 반응을 증가시키는 데 사용될 수 있다.

[0184] 일부 실시양태에서, PGA 변이체는 효소를 발현하는 세포의 형태로, 조 추출물로서, 또는 단리된 또는 정제된 제제로서 제조되고, 사용된다. 일부 실시양태에서, PGA 변이체는 분말 형태(예컨대, 아세톤 분말)인, 동결건조물로서 제조되거나, 또는 효소 용액으로 제조된다. 일부 실시양태에서, PGA 변이체는 실질적으로 순수한 제제 형태이다.

[0185] 일부 실시양태에서, PGA 폴리펩티드는 임의의 적합한 고체 기판에 부착된다. 고체 기판으로는 고체상, 표면, 및/또는 막을 포함하나, 이에 제한되지 않는다. 고체 지지체로는 유기 중합체, 예컨대, 폴리스티렌, 폴리에틸렌, 폴리프로필렌, 폴리플루오로에틸렌, 폴리에틸렌옥시, 및 폴리아크릴아미드 뿐만 아니라, 그의 공중합체 및 그래프트를 포함하나, 이에 제한되지 않는다. 고체 지지체는 또한 무기물, 예컨대, 유리, 실리카, 공극 조절형 유리(CPG: controlled pore glass), 역상 실리카 또는 금속, 예컨대, 금 또는 백금일 수 있다. 기판의 입체형태는 비드, 구체 입자, 과립, 겔, 막 또는 표면의 형태일 수 있다. 표면은 평면, 실질적으로 평면 또는 비평면일 수 있다. 고체 지지체는 다공성이거나, 또는 비다공성일 수 있고, 팽윤성 또는 비팽윤성 특징을 가질 수 있다. 고체 지지체는 웰, 함몰형, 또는 다른 용기, 베쓸, 지형, 또는 위치 형태로 구성될 수 있다. 다수의 지지체가 시약의 로봇식 전달을 다룰 수 있거나, 또는 검출 방법 및/또는 장비에 의해 다룰 수 있는, 다양한 위치의 어레이상에 배치될 수 있다.

[0186] 일부 실시양태에서, 면역학적 방법이 PGA 변이체를 정제하는 데 사용된다. 한 접근법에서, 통상의 방법을 사용하여 변이체 PGA 폴리펩티드에 대하여(예컨대, 서열 번호: 4, 8, 14, 300, 1036, 1194, 1262, 및/또는 12882 중 임의의 것을 포함하는 폴리펩티드, 및/또는 그의 면역원성 단편에 대하여) 생성된 항체를 비드 상에 고정화시키고, 변이체 PGA가 결합하는 조건하에서 세포 배양 배지와 혼합하고, 침전시킨다. 관련된 접근법에서, 면역크로마토그래피가 사용된다.

[0187] 일부 실시양태에서, 변이체 PGA는 비효소 부분을 포함한 융합 단백질로서 발현된다. 일부 실시양태에서, 변이체 PGA 서열은 정제 용이 도메인에 융합된다. 본원에서 사용되는 바, "정제 용이 도메인"이라는 용어는 융합되는 폴리펩티드의 정제를 매개하는 도메인을 지칭한다. 적합한 정제 도메인으로는 금속 킬레이팅 펩티드, 고정된 금속상에서 정제를 가능하게 하는, 히스티딘-트립토판 모듈, 글루타티온에 결합하는 서열(예컨대, GST), 헤마글루티닌(HA) 태그(인플루엔자 헤마글루티닌 단백질로부터 유래된 에피토프에 상응; 예컨대, 문헌 [Wilson et al., Cell 37:767 [1984] 참조), 말토스 결합 단백질 서열, FLAGS 확장/친화성 정제 시스템(예컨대, Immunex Corp로부터 입수가능한 시스템)에서 이용되는 FLAG 에피토프 등을 포함하나, 이에 제한되지 않는다. 본원에 기술된 조성물 및 방법에서의 사용이 고려되는 한 발현 벡터는 엔테로키나제 절단 부위에 의해 이격된 폴리히스티딘 영역에 융합된 본 발명의 폴리펩티드를 포함하는 융합 단백질의 발현을 제공한다. 히스티딘 잔기는 IMIAC(고정된 금속 이온 친화성 크로마토그래피: immobilized metal ion affinity chromatography; 예컨대, 문헌 [Porath *et al.*, Prot. Exp. Purif., 3:263-281 [1992]] 참조) 상에서 정제를 용이하게 하는 한편, 엔테로키나제 절단 부위는 융합 단백질로부터 변이체 PGA 폴리펩티드를 분리시키기 위한 수단을 제공한다. pGEX 벡터(Promega)는 글루타티온 S-트랜스퍼라제(GST: glutathione S-transferase)와의 융합 단백질로서 외래 폴리펩티드를 발현시키는 데 사용될 수 있다. 일반적으로, 상기 융합 단백질은 가용성이고, 리간드-아가로스 비드(예컨대, GST-융합체의 경우 글루타티온-아가로스)에 흡착 후, 유리 리간드 존재에서 용출시킴으로써 용해된 세포로부터 쉽게 정제될 수 있다.

[0188] **실험부**

[0189] 본 개시내용의 다양한 특징 및 실시양태가 하기의 대표적인 실시예에서 예시되지만, 이는 예시를 위한 것이고, 제한하는 것이 아니다.

[0190] 하기 실험 개시내용에서, 하기 약어가 적용된다: ppm(백만분율: parts per million); M(몰 농도); mM(밀리몰 농도), uM 및 μM(마이크로몰 농도); nM(나노몰 농도); mol(몰수); gm 및 g(그램); mg(밀리그램); ug 및 μg(마이크로그램); L 및 ℓ(리터); ml 및 mL(밀리리터); cm(센티미터); mm(밀리미터); um 및 μm(마이크로미터); sec(초); min(s)(분); h 및 hr(시간); U(유니트); MW(분자량: molecular weight); rpm(분당 회전수: rotations

per minute); ℃(섭씨 온도); RT(실온: room temperature); CDS(코딩 서열: coding sequence); DNA(데옥시리보핵산); RNA(리보핵산); TB(테리픽 브로쓰(Terrific Broth); 12 g/L 박토-트립톤, 24 g/L 효모 추출물, 4 mL/L 글리세롤, 65 mM 인산칼륨, pH 7.0, 1 mM MgSO4); CAM(클로람페니콜); PMBS(폴리믹신 B 술페이트: polymyxin B sulfate); IPTG(이소프로필 티오갈락토시드: isopropyl thiogalactoside); TFA(트리플루오로아세트산); HPLC(고성능 액상 크로마토그래피); FIOPC(양성 대조군 대비 개선 배수: fold improvement over positive control); HTP(고처리량: high throughput); LB(루리아 브로쓰: Luria broth); 코데시스(Codexis)(Codexis, Inc.: 미국 캘리포니아주 레드우드 시티 소재); 시그마-알츠리치(Sigma-Aldrich)(Sigma-Aldrich: 미국 미주리주 세인트 루이스 소재); 밀리포어(Millipore)(Millipore, Corp.: 미국 매사추세츠주 빌러리카 소재); 디프코(Difco)(Difco Laboratories, BD Diagnostic Systems: 미국 미시간주 디트로이트 소재); 다이셀(Daicel)(Daicel: 미국 펜실베니아주 웨스트체스터 소재); 제네티스(Genetix)(Genetix USA, Inc.: 미국 오리건주 비버턴 소재); 몰레큘라 디바이시스(Molecular Devices)(Molecular Devices, LLC: 미국 캘리포니아주 서니배일 소재); 어플라이드 바이오시스템즈(Applied Biosystems)(Applied Biosystems, Life Technologies, Corp의 지부: 미국 뉴욕주 그랜드 아일랜드 소재), 애질런트(Agilent)(Agilent Technologies, Inc.: 미국 캘리포니아주 산타클라라 소재); 써모 사이언티픽(Thermo Scientific)(Thermo Fisher Scientific의 지부: 미국 매사추세츠주 월섬 소재); 인폴스(Infors)(Infors-HT: 스위스 보트민겐/바젤 소재); 코닝(Corning)(Corning, Inc.: 미국 캘리포니아주 팔로 알토 소재); 및 바이오-래드(Bio-Rad Laboratories: 미국 캘리포니아주 허큘리스 소재); 마이크로플루이딕스(Microfluidics)(Microfluidics Corp.: 미국 매사추세츠주 뉴턴 소재).

[0191] **실시예 1**

[0192] **재조합 PGA 유전자를 함유하는 이. 콜라이 발현 숙주**

[0193] 본 발명의 변이체를 제조하는 데 사용된 초기 PGA 효소는 코덱스® 아실라제 패널(Codex® Acylase Panel)(Codexis), 또는 공동 소유의 미국 가특허 출원 제62/158,118호에 개시된 변이체로부터 수득되었다. PGA 패널 플레이트는 야생형 클루이베라 시트로필라 PGA와 비교하여, 개선된 특성을 가지는 조작된 PGA 폴리펩티드의 콜렉션을 포함한다. 야생형 PGA 유전자는 54 aa 스페이서 영역에 의해 연결된 알파 서브유니트(23.8 KDa) 및 베타 서브유니트(62.2 KDa)로 구성된 이종이량체이다. 스페이서 영역의 존재에 기인하여, 활성 단백질 형성을 위해 자가 프로세싱 단계가 요구된다. 야생형 유전자는 스페이서 영역을 제거하도록 변형됨에 따라 자가 프로세싱 단계가 없어졌다. 코덱스® 아실라제 패널(Codexis)은 스페이서 영역이 결여된 PGA 변이체를 함유한다(예컨대, 미국 특허 출원 공개 2010/0143968 A1 참조). PGA-코딩 유전자는 lacI 리프레서의 제어하에 있는 lac 프로모터에 작동적으로 연결된 발현 벡터 pCK110900에 클로닝되었다(예컨대, 미국 특허 출원 공개 번호 2006/0195947의 도 3 참조). 발현 벡터는 또한 P15a 복제 기점 및 클로람페니콜 내성 유전자를 함유한다. 당업계에 공지된 표준 방법을 사용하여, 생성된 플라스미드를 이. 콜라이 W3110에 형질전환시켰다. 당업계에 공지된 바와 같이(예컨대, 미국 특허 번호 8,383,346 및 WO2010/144103 참조), 세포에 대해 클로람페니콜 선별을 수행하여 형질전환체를 단리시켰다.

[0194] **실시예 2**

[0195] **HTP PGA 함유 습윤 세포 펠릿 제조**

[0196] 단일클론 콜로니로부터의 재조합 PGA 코딩 융전자를 함유하는 이. 콜라이 세포를 96 웰 얕은 웰 마이크로타이터 플레이트의 웰 중 1% 글루코스 및 30 ㎍/mL 클로람페니콜을 함유하는 180 ㎕ LB에 접종하였다. 플레이트를 O_2 투과성 씰(permeable seal)로 밀봉하고, 배양물을 30℃, 200 rpm 및 85% 습도에서 밤새도록 성장시켰다. 이어서, 10 ㎕의 각 세포 배양물을 390 mL TB 및 30 ㎍/mL CAM을 함유하는 96 웰 깊은 웰 플레이트의 웰로 옮겼다. 깊은 웰 플레이트를 O_2 투과성 씰로 밀봉하고, OD600 0.6-0.8에 도달할 때까지 30℃, 250 rpm 및 85% 습도에서 인큐베이션시켰다. 이어서, 세포 배양물을 1 mM의 최종 농도로 IPTG에 의해 유도시키고, 원래 사용된 것과 동일한 조건하에서 밤새도록 인큐베이션시켰다. 이어서, 세포를 4,000 rpm으로 10 min 동안 원심분리를 사용하여 펠릿화시켰다. 상청액을 폐기하고, 펠릿은 용해 전에 -80℃에서 냉동시켰다.

[0197] **실시예 3**

[0198] **HTP PGA 함유 세포 용해물 제조**

[0199] 먼저, 실시예 2에 기술된 바와 같이 제조된 각 웰 중의 세포 페이스트에 10 mM 트리스-HCl 완충제, pH 7.5, 1 mg/mL 리소자임, 및 0.5 mg/mL PMBS를 함유하는 200 ㎕의 용해 완충제를 첨가하였다. 세포를 실온에서 2시간 동

안 벤치 탑 진탕기 상에서 진탕시키면서 용해시켰다. 이어서, 플레이트를 4℃에서 15 min 동안 4,000 rpm으로 원심분리하였다. 투명한 상청액을 그의 활성 수준을 측정하기 위해 생물촉매 반응에 사용하였다.

[0200] **실시예 4**

[0201] **진탕 플라스크(SF: Shake Flask) 배양물로부터의 동결건조된 용해물 제조**

[0202] 상기에 기술된 바와 같이 성장시킨 선택된 HTP 배양물을 1% 글루코스 및 30 ㎍/ml CAM을 포함하는 LB 아가 플레이트 상에 플레이팅하고, 37℃에서 밤새도록 성장시켰다. 각 배양물로부터의 단일 콜로니를 1% 글루코스 및 30 ㎍/ml CAM을 포함하는 6 ml의 LB로 옮겼다. 배양물을 30℃에서 18 h 동안 250 rpm으로 성장시켰고, 30 ㎍/ml CAM을 함유하는 250 ml의 TB에 대략 1:50으로, 최종 OD_{600}이 0.05가 될 때까지 계대배양하였다. 배양물을 OD_{600}이 0.6-0.8이 될 때까지, 대략 195분 동안 30℃, 250 rpm으로 성장시키고, 1 mM IPTG로 유도시켰다. 이어서, 배양물을 20 h 동안 30℃, 250 rpm으로 성장시켰다. 배양물을 4,000 rpm x 20 min 동안 원심분리시켰다. 상청액을 폐기하고, 펠릿을 30 ml의 20 mM TRIS-HCl, pH 7.5 중에 재현탁시켰다. 세포를 펠릿화(4,000 rpm x 20 min)시키고, -80℃에서 120분 동안 냉동시켰다. 냉동된 펠릿을 30 ml의 20 mM TRIS-HCl pH 7.5 중에 재현탁시키고, 마이크로플루이다이저(Microfluidizer) 시스템(Microfluidics)을 사용하여 18,000 psi에서 용해시켰다. 용해물을 펠릿화(10,000 rpm x 60 min)시키고, 상청액을 냉동 및 동결건조시켜 진탕 플라스크(SF) 효소를 생성하였다.

[0203] **실시예 5**

[0204] **B29 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0205] **서열 번호: 8 대비 개선**

[0206] B29 탈아실화된 생성물의 제조를 위해 미국 가특허 출원 제62/158,118호에 개시된 변이체에 대해 스크리닝한 후, 서열 번호: 8을 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다. 5 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 200 mM 트리스 완충제 pH=8.3 및 40 ㎕ 조용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 3시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론(Thermotron)® 진탕기 중 100 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴 또는 디메틸아세트아미드로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 물로 2배 희석시키고, 분석을 위해 HPLC에 적재하였다.

[0207] 서열 번호: 8 대비 활성(활성 FIOP)은 서열 번호: 8에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 5.1에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 5

표 5.1 서열 번호: 8 대비 변이체의 활성

서열 번호: : (nt/aa)	아미노산 차이 (서열 번호: 8 대비)	활성 FIOP [1] (서열 번호: 8 대비)
9/10	G71C;D74G	+
11/12	Y27T;G71H;D74G;D484N;Q547K;Y584F;M697L	+
13/14	Y27T;V28A;G71H;D74G;Q547K	+
39/40	L253Y	+
41/42	Y27T	+
29/30	S386G;K390S	+
17/18	L387K;K390S	+
81/82	A474C	+
45/46	S386A;K390S	+
69/70	S386H	+
15/16	S704N	+
27/28	F254N	+
63/64	A470C	+
31/32	A373R	+
23/24	T352K	+
59/60	L253H	+
37/38	A616Y	+
55/56	S372L	+
19/20	A451K	+
77/78	I708L	+
43/44	F256Y	+
35/36	L387R;K390S	+
21/22	D623Q	+
47/48	A467W	+
53/54	D623K	+
73/74	N348H	+
51/52	F254K	+
49/50	S706T	+
33/34	S374T	+
83/84	Q380M	+
75/76	T129W	+
67/68	Q380Y;N457L	+
57/58	A470E	+
61/62	N457A	+
25/26	D623A	+
65/66	N457Q	+
79/80	F256S	+
71/72	A373K	+

[1] 활성 증가 수준은 서열 번호: 8의 참조 폴리펩티드 대비로 측정되었고,
이는 하기와 같이 정의되었다: "+" 1배 초과 2.0배 미만의 활성 증가;
"++" 2.0배 초과 3배 미만의 활성 증가; "+++" 3배 초과 내지 10배 미만의 활성 증가;
"++++" 10배 초과.

[0208]

[0209] **실시예 6**

[0210] **B29 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0211] **서열 번호: 14 대비 개선**

[0212] 실시예 5에 기술된 변이체에 대해 스크리닝한 후, 서열 번호: 14를 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0213] 10 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 200 mM 트리스 완충제 pH=8.3 및 20 ㎕ 조 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 24시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론 진탕기 중 100 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴 또는 디메틸아세트아미드로 켄

칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 물로 2배 희석시키고, 분석을 위해 HPLC에 적재하였다.

[0214] 서열 번호: 14 대비 활성(활성 FIOP)은 서열 번호: 14에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 6.1에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 6

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
419/420	N185D	+
433/434	T560G	+
443/444	A517K	+
415/416	G415H	+
441/442	G444K	+
417/418	G444T	+
421/422	R748D	+
439/440	G444R	+
447/448	T443D	+
423/424	G444S	+
427/428	S492G/G493C	+
431/432	N9D	+
437/438	G444Q	+
429/430	R748S	+
435/436	K723D	+
445/446	R748E	+

[0215]

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
425/426	G444L	+
165/166	N9S;K103E;W119Y;T131D;Q233K;T269R;K304Q;G444N;N494D;S646D	+
177/178	K103E;G444N;N494D;S646D	+
119/120	K103E;W119Y;T131D;Q233K;K273A;K304Q;A324T;Q432E;G444N;N494D;S646D	+
211/212	K103E;W119Y;Q233K;E312A;S646D	+
207/208	N9S;K103E;W119Y;T131D;K304Q;A324T;Q432E;G444N;N494D;S646D	+
149/150	W119Y;Q233K;K304Q;E312A;A324T;Q432E;G444N;S646D	+
175/176	K103E;T131D;Q233K;K304Q;A324T;G444N;S646D	+
85/86	K103E;W119Y;N494D;S646D;K661Q	+
111/112	N9S;W119Y;T131A;Q233K;N494D;S646D	+
125/126	K103E;W119Y;Q233K;K304Q;S646D	+
173/174	N9S;K103E;W119Y;Q233K;S646D	+
215/216	K103E;Q233K;K273A;E312A;Q432E;G444N;S646D	+
133/134	N9S;W119Y;Q233K;N494D;S646D	+
155/156	W119Y;K273A;A324T;G444N;N494D;S646D	+
181/182	N9S;W119Y;T131A;Q233K;K304Q;G444N;S646D	+
121/122	K103E;W119Y;T131A;Q233K;K304Q;E312A;Q432E;N494D;S646D;K661Q	+
163/164	W119Y;Q233K;K304Q;S646D	+
115/116	N9S;W119Y;K304Q;G444N;N494D;S646D	+
109/110	N9S;W119Y;Q233K;T269R;K273A;K304Q;E312A;Q432E;G444N;S646D	+
123/124	W119Y;E312A;G444N;S646D	+
113/114	N9S;W119Y;T131A;E312A;G444N;S646D	+
143/144	K103E;E312A;G444N;S646D	+
103/104	K103E;W119Y;S646D	+
135/136	W119Y;Q233K;S646D	+
129/130	K103E;W119Y;Q233K	+
167/168	W119Y;T131A;G444N;S646D;K661Q	+
157/158	W119Y;Q432E;G444N;S646D	+
189/190	K103E;T269R;K273A;G444N;S646D	+
159/160	N9S;T131A;Q233K;T269R;K273A;E312A;Q432E;G444N;S646D	+
183/184	K103E;K273A;K304Q;A324T;G444N;N494D	+
105/106	E312A;G444N;S646D	+
127/128	N9S;Q233K;N494D;S646D	+
221/222	N9S;Q233K;K304Q;N494D;S646D	+
191/192	T131D;K273A;Q432E;G444N;N494D;S646D	+
219/220	N9S;Q432E;G444N;N494D;S646D	+
171/172	N9S;Q233K;K273A;K304Q;N494D;S646D	+
169/170	K103E;Q233K;K273A;E312A;A324T;Q432E;G444N;S646D	+

[0216]

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
97/98	N9S;K103E;Q233K;N494D	+
201/202	W119Y;T269R;K273A;E312A;Q432E;G444N;S646D	+
187/188	T131A;Q233K;K304Q;G444N	+
101/102	N9S;K103E;W119Y;N494D	+
197/198	K103E;T131D;T269R;K273A;G444N;S646D	+
91/92	N9S;W119Y;T131D;Q233K;N494D;K661Q	+
205/206	K103E;W119Y;T131A;T269R;E312A;N494D;S646D	+
223/224	N9S;K103E;W119Y;T131A;Q233K;E312A;A324T;Q432E;G444N;N494D	+
213/214	N9S;W119Y;T131A;Q432E;G444N;S646D	+
145/146	G444N;N494D	+
95/96	W119Y;T131A;N494D	+
93/94	N9S;K103E;K304Q;Q432E;G444N;S646D	+
185/186	K304Q;E312A;G444N;S646D	+
147/148	W119Y;T131A;S646D	+
139/140	G444N;S646D	+
89/90	K273A;E312A;G444N;S646D	+
199/200	W119Y;Q233K;E312A	+
137/138	T131A;Q233K;K273A;S646D	+
153/154	N9S;E312A;G444N;S646D	+
161/162	N9S;W119Y;T131D;Q233K	+
195/196	E312A;S646D	+
193/194	N9S;K103E;T269R;K304Q;A324T;N494D;S646D	+
107/108	W119Y;T131D;K304Q;Q432E;G444N;S646D;K661Q	+
131/132	W119Y;T131D;G444N	+
209/210	T131A;Q233K;Q432E;S646D	+
99/100	N9S;Q233K;E312A;Q432E;S646D	+
141/142	N9S;K103E;Q233K;E312A;S646D	+
117/118	K103E;W119Y;Q233K;K273A;Q432E	+
179/180	Q233K;T269R;K304Q;E312A;A324T;Q432E;G444N;S646D	+
217/218	N9S;K103E;W119Y;T131A;A324T;Q432E;N494D;S646D	+
203/204	N9S;N494D;S646D	+
87/88	N9S;K103E;Q233K;Q432E;S646D	+
151/152	W119Y;T269R;K273A;E312A;A324T;N494D;S646D	+
237/238	L253Y;F256Y;T352K;A451K;	+++
299/300	L253Y;T352K;A373R;S374T;A451K;A616Y	+++
271/272	L253H;F256Y;T352K;A373R;S374T;A616Y	++
321/322	F256Y;S374T;Q380L;A451K;A616Y	++
307/308	Q380L;A451K;A616Y	++
323/324	L253H;T352K;A451K;A616Y	++
243/244	L253Y;F256Y;T352K;S374T;Q380L;A451K	++
293/294	F254N;A373R;S374T;A451K	++
273/274	T352K;A373R;S374T;A451K	++
337/338	L253Y;T352K;A373R;S374T;A451K	++

[0217]

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
227/228	L253H;A451K;N457S	++
325/326	L253Y;F256Y;T352K;S374T;A451K	++
333/334	L253H;T352K;S374T;A616Y	++
363/364	L253Y;A373R;S374T;A451K;A616Y	++
275/276	T352K;S374T;A451K	++
331/332	L253Y;F254N;T352K;S374T;Q380L	++
343/344	S374T;A451K;A616Y	++
295/296	A451K;A616Y	++
351/352	T352K;S374T;Q380L;A451K;A616Y	++
367/368	T352K;Q380L;A451K;A616Y	++
349/350	L253Y;T352K;S374T;A616Y	++
401/402	L253H;F256Y;T352K;Q380L;A451K;A616Y	++
289/290	T352K;A451K;A616Y	++
381/382	L253Y;F256Y;A373R	++
383/384	L253H;F256Y;S374T;A616Y	++
253/254	S374T;Q380L;A451K	++
335/336	S374T;Q380L;A451K;D623N	++
355/356	L253Y;F256Y;T352K;Q380L	++
405/406	T352K;S374T;A616Y	++
225/226	F254N;T352K;Q380L;A451K	++
231/232	A373R;S374T;A451K	++
379/380	F254N;A616Y	++
393/394	L253H;F256Y;Q380L;A451K;A616Y	++
399/400	F254N;A373R;S374T;Q380L;A451K	++
411/412	L253H;F256Y;T352K;S374T;Q380L;A451K	++
263/264	F254N;F256Y;S374T;A451K	++
341/342	S374T;A616Y	++
283/284	L253H;S374T;A451K	++
375/376	F256Y;S374T;A616Y	++
339/340	F254N;T352K;A451K	++
407/408	L253Y;F256Y;Q380L	++
373/374	F256Y;T352K;S374T	++
409/410	L253H;S374T;A451K;D623Q	++
285/286	L253Y;T352K;D623N	++
279/280	Q380L;A451K;D623A	++
269/270	F254N;A451K	++
257/258	T352K;Q380L;A451K;D623Q	++
403/404	T352K;A373R;A451K	++
359/360	T352K;S374T	++
345/346	Q380L;A616Y	++
305/306	L253H;F256Y	++
245/246	S374T;A451K	++
377/378	L253Y;F256Y	++
385/386	T352K;S374T;Q380L	++
365/366	L253H;A373R;A451K	++
287/288	L253Y;Q380L	++

[0218]

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
291/292	Q380L;A451K	++
353/354	F254N;F256Y;Q380L;A451K;A616Y	++
313/314	F254N;S374T	++
309/310	F254N;S374T;Q380L	++
239/240	T352K;Q380L;A616Y	++
361/362	T352K;Q380L;A451K	++
387/388	L253H;F256Y;S374T;A451K	++
249/250	A373R;S374T	++
371/372	L253H;A451K	++
255/256	L253Y;F256Y;Q380L;A451K;H546Y;A616Y	+
327/328	T352K;A616Y	+
267/268	A616Y	+
347/348	F256Y;T352K;Q380L;A451K;A616Y	+
329/330	S374T;Q380L	+
311/312	S374T;D623Q	+
281/282	F254N;F256Y;A373R;S374T;Q380L;A451K	+
235/236	T352K;A451K	+
319/320	T352K;A373R;Q380L;A451K;A616Y	+
229/230	D623A	+
413/414	Q380L;A616Y;D623Q	+
265/266	A373R;A451K	+
251/252	S374T	+
395/396	F254N;F256Y;T352K;A451K	+
397/398	A451K;D623N	+
247/248	F254N;F256Y;S374T	+
233/234	L253H	+
317/318	F254N;A255E;T352K	+
369/370	A28S;S374T;Q380L	+
301/302	F254N;T352K;Q380L	+
261/262	F254N;Q380L	+
241/242	A451K	+
277/278	T352K	+
259/260	T352K;Q380L	+
389/390	D623N	+
391/392	D623Q	+
303/304	T352K;A373R;Q380L;A451K	+
297/298	Q380L	+
357/358	F254N;F256Y;A451K	+
315/316	A373R;A616Y	+
451/452	N457Q;A470C	+
455/456	T129W;F254K;N348H;N457Q;S704N	+
467/468	N348H;S372L;A470E;D623K;I708L	+
457/458	N457Q;S704N;I708L	+
483/484	T129W;D623K	+
453/454	N457Q	+
485/486	T129W;N348H	+

[0219]

표 6.1 서열 번호: 14 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 14 대비)	활성 FIOP [1] (서열 번호: 14 대비)
461/462	N348H	+
449/450	N348H;S704N;I708L	+
459/460	T129W;Q380M;A470E	+
469/470	T129W;N457Q;A470C;A474C	+
471/472	T129W;N348H;A470E;D623K;S704N;S706T;I708L	+
475/476	T129W;N348H;A467W;A470C;S704N;I708L	+
477/478	S372L;N457Q;A470E;D623K	+
479/480	D623K	+
481/482	A470C;I708L	+
465/466	T129W;N348H;A470E;D623K;S704N;S706T	+
463/464	T129W;A470E	+
473/474	Q380M;D623K	+

[1] 활성 증가 수준은 서열 번호: 14의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가; "++" = 2.0배 초과 3배 미만의 활성 증가; "+++" = 3배 초과 내지 10배 미만의 활성 증가; "++++" = 10배 초과.

[0220]

[0221] **실시예 7**

[0222] **B29 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0223] **서열 번호: 300 대비 개선**

[0224] 실시예 6에 기술된 변이체에 대해 스크리닝한 후, 서열 번호: 300을 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0225] 50 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 200 mM 트리스 완충제 pH=8.3 및 2.5 ㎕ 조 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 24시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론 진탕기 중 100 rpm에서 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴 또는 디메틸아세트아미드로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 물로 2배 희석시키고, 분석을 위해 HPLC에 적재하였다.

[0226] 서열 번호: 300 대비 활성(활성 FIOP)은 서열 번호: 300에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 7.1에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 7

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
837/838	N9D;N185D;G415H;G444T;A517K;T560G;K723D;R748E	+++
813/814	N9D;N185D;G415H;T443D;G444R;A517K;K723D;R748D	+++
775/776	N9D;G415H;T443D;T560G;K723D;R748D	+++
839/840	N9D;G415H;G444L;T560G;K723D;R748E	+++
719/720	N9D;G415H;T443D;G444R;T560G;K723D;R748E	+++
797/798	G415H;T443D;A517K;T560G;K723D	+++
695/696	N9D;G415H;T443D;G444T;A517K;T560G;K723D	+++
767/768	N9D;N185D;G415H;G444S;K723D;R748E	+++
597/598	N9D;N185D;G415H;T443D;G444T;A517K;T560G	+++
561/562	N9D;N185D;G415H;G444L;A517K;T560G;K723D;R748S	+++
827/828	N185D;G415H;T443D;G444R;A517K;T560G	+++
771/772	N185D;G415H;G444T;T560G	+++
773/774	N9D;N185D;T443D;G444K;T560G;K723D	+++
765/766	G415H;T443D;G444T;T560G	+++
769/770	G415H;G444Q;T560G;K723D	+++
791/792	N9D;G415H;A517K;T560G;K723D;R748D	+++
783/784	G415H;A517K;T560G;K723D;R748D	+++
673/674	N185D;G415H;T443D;G444T;A517K	++
545/546	N9D;G415H;G444Q;A517K;T560G;K723D;R748S	++
727/728	N9D;N185D;G415H;T443N;G444K;A517K;R748E	++
599/600	N9D;G415H;G444L;A517K;T560G;K723D;R748D	++
633/634	N9D;G415H;T443D;G444S;A517K;T560G	++
651/652	N9D;G415H;T443D;G444T;A517K;R748S	++
683/684	N9D;G415H;G444T;A517K;T560G;K723D	++
817/818	G415H;G444S;A517K;K723D;R748E	++
671/672	N9D;G415H;G444Q;T560G;K723D	++
557/558	N9D;N185D;G415H;G444K;A517K;K723D;R748E	++
627/628	N185D;G415H;G444R;A517K;T560G;R748D	++
699/700	N9D;G415H;T443D;G444K;A517K;T560G	++
679/680	N9D;G415H;A517K;T560G;K723D;R748E	++
569/570	N9D;T443D;G444K;T560G;K723D;R748D	++
589/590	G415H;G444Q;A517K;T560G;K723D;R748S	++
573/574	G415H;G444S;A517K;T560G;K723D	++
799/800	N9D;N185D;G415H;G444K;A517K;R748D	++
525/526	G415H;T443D;G444T;A517K;R748E	++
639/640	G415H;T443D;A517K;K723D	++
807/808	N9D;N185D;G444Q;A517K;T560G;K723D	++
749/750	N9D;N185D;G444T;A517K;T560G;K723D	++
619/620	N9D;T443D;G444K;A517K;T560G;K723D	++
543/544	N185D;G415H;T560G;K723D	++
779/780	N9D;G415H;G444L;K723D;R748S	++
707/708	N9D;N185D;G415H;G444L;A517K;T560G	++
725/726	N9D;N185D;T443D;G444K;A517K;T560G	++
523/524	N9D;G415H;G444T;T560G;S665R;K723D;R748S	++
713/714	G415H;G444S;T560G;R748E	++
587/588	N9D;N185D;T443D;G444S;K723D	++

[0227]

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
539/540	N9D;N185D;G415H;G444Q;T560G	++
551/552	G415H;G444Q;A517K;T560G;R748S	++
553/554	N9D;G415H;G444T;K723D;R748E	++
741/742	N9D;G415H;G444R;A517K;T560G;R748E	++
595/596	N9D;G415H;T443D;G444R;A517K;R748E	++
655/656	N9D;N185D;G415H;A517K;K723D	++
641/642	N9D;N185D;G444Q;A517K;T560G;R748D	++
751/752	G415H;G444S;T560G	++
491/492	N9D;G415H;T443D;T560G	++
823/824	N9D;G444L;A517K;T560G;K723D;R748E	++
717/718	N9D;N185D;G415H;A517K;T560G	++
611/612	N185D;G415H;K723D;R748S	++
593/594	N9D;G415H;G444T;T560G	++
745/746	N9D;N185D;A517K;T560G;K723D;R748E	++
575/576	G415H;T560G;K723D	++
643/644	N9D;T443D;G444R;T560G;K723D	++
609/610	N9D;T443D;G444T;A517K;T560G	++
515/516	G415H;A517K;T560G;R748E	++
489/490	N9D;G415H;G444K;A517K;T560G;R748S	++
583/584	N9D;G415H;G444S;T560G	++
601/602	N185D;G444R;A517K;T560G;K723D;R748S	++
715/716	N185D;G415H;T560G	++
735/736	N185D;G415H;G444R;A517K;R748S	++
513/514	N9D;G415H;A517K;T560G;R748E	++
511/512	N9D;G61D;G444S	++
617/618	G415H;G444K;K723D	++
733/734	N9D;N185D;G444L;T560G;K723D	++
675/676	G415H;K723E;R748E	++
723/724	N9D;G415H;G444R;T560G	++
665/666	N185D;T443D;G444R;T560G	++
607/608	N9D;G444N;A517K;T560G;K723D;R748E	++
653/654	N9D;N185D;G415H;A517K;R748S	++
647/648	N9D;G444Q;A517K;T560G;K723D	++
509/510	N9D;N185D;G444S;A517K;K723D;R748S	++
691/692	N9D;N185D;G415H;R748E	++
787/788	N9D;G415H;G444Q;A517K	++
549/550	G444L;A517K;T560G;K723D;R748S	++
487/488	N185D;A517K;T560G;K723D	++
677/678	T443D;G444T;K723D	++
681/682	T443D;G444K;A517K;R748E	++
649/650	N9D;N185D;G444L;T560G;R748S	++
785/786	N9D;G415H;G444K	++
531/532	N9D;N185D;G415H;G444Q	++
621/622	G415H;K723D;R748S	++
819/820	N185D;G444L;A517K;T560G	++
795/796	G415H;G444T	++

[0228]

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
625/626	N9D;G415H;T560G	++
687/688	G444S;A517K;K723D;R748E	++
585/586	N9D;G444K;T560G;K723D	++
499/500	N9D;T443D;G444T;A517K;R748S	++
541/542	N9D;N185D;G444Q;A517K;T560G	++
753/754	N9D;N185D;G444S;T560G	++
645/646	N9D;N185D;G444L;A517K;T560G	++
581/582	N185D;G444S;A517K;K723D	++
659/660	N9D;G415H;G444L;A517K	++
535/536	T443D;G444S;T560G	++
801/802	N9D;N185D;G444S;K723D	++
579/580	N9D;T443D;G444K;T560G	++
669/670	G444T;T560G;K723D	++
689/690	G415H;G444L;A517K	++
763/764	N9D;N185D;T443D;G444R;A517K	++
777/778	N185D;T560G;K723D	++
757/758	N9D;T443D;K723D	++
637/638	N9D;T443D;G444S;A517K	++
635/636	N9D;G444L;T560G;K723D	++
503/504	N9D;G415H;G444S;A517K	++
815/816	N185D;T560G;R748E	++
825/826	N9D;Q168R;N185D;A517K;T560G;R748S	++
781/782	G444L;T560G;K723D	++
667/668	N9D;G444T;A517K;T560G	++
743/744	N9D;G444L;T560G;R748E	++
711/712	N9D;T443D;A517K;R748E	++
563/564	G444Q;T560G;K723D	++
603/604	N9D;N185D;G415H	++
821/822	G415H;G444L	++
661/662	N9D;G415H;G444R;A517K	++
623/624	N9D;A517K;T560G;K723D	++
731/732	G415H;R748E	++
663/664	N185D;T560G;R748S	++
537/538	N9D;T560G;K723D;R748S	++
793/794	G444Q;T560G	++
567/568	N9D;G444L;T560G;R748S	+
519/520	N9D;G444S;T560G;R748E	+
693/694	N9D;G415H;R748S	+
521/522	N9D;G444Q;A517K;K723D	+
755/756	N185D;G444R;T560G	+
709/710	N9D;G415H;A517K	+
615/616	N9D;A517K;T560G;R748E	+
547/548	G444T;A517K;T560G	+
729/730	N9D;A517K;T560G;R748D	+
803/804	A517K;T560G;R748E	+
555/556	G444K;A517K;T560G	+

[0229]

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
497/498	N9D;G444K;A517K;T560G	+
831/832	N9D;N185D;G444K	+
591/592	G415H;A517K	+
613/614	G444K;A517K;R748E	+
737/738	N185D;T560G	+
739/740	G444S;K723D	+
493/494	G444S;T560G;R748S	+
835/836	N9D;N185D;R748E	+
829/830	N9D;G444K;R748S	+
809/810	G415H	+
701/702	N9D;G444L;T560G	+
685/686	T443D;A517K	+
705/706	N9D;G444S;K723D	+
501/502	T443D;G444S	+
761/762	N9D;N185D;A517K	+
629/630	A517K;T560G	+
805/806	N9D;A517K;K723D	+
833/834	G444K;R748S	+
505/506	N9D;T443D;G444R;A517K	+
507/508	G444R;A517K;T560G	+
747/748	A517K;K723D	+
571/572	N9D;G444Q;A517K	+
517/518	K723D;R748D	+
533/534	N185D;G444K;K446N;A517K;T560G	+
565/566	N9D;G444L;R748E	+
495/496	T443D;G444K;A517K;T560G;K723D;R748S	+
657/658	N9D;K15M;G444L;K723D	+
631/632	N9D;G444T	+
697/698	N9D;A517K;R748S	+
811/812	N9D;N185D	+
529/530	N9D;K723D	+
605/606	A517K;R748E	+
789/790	K723D	+
527/528	G415H;A517K;T560G	+
559/560	T560G	+
721/722	G444K	+
759/760	G444R;A517K	+
577/578	N9D;A517K	+
703/704	A517K;R748S	+
903/904	K103E;W119Y;N348H;N457Q;N494D	+++
897/898	K103E;W119Y;F256R;N348H;G444N;N494D;S646D	++
877/878	K103E;T129W;F254N;G444N;N457Q;N494D	++
943/944	K103E;W119Y;N348H;N457Q	++
895/896	K103E;W119Y;N457Q	++
855/856	W119Y;T129W;F256R;N348H;N457Q	++
945/946	W119Y;T129W;F254N;N457Q;N494D	++

[0230]

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
935/936	K103E;F256R;N457Q	++
881/882	W119Y;F256R;N348H;N494D	++
939/940	N348H;N457Q	++
911/912	K103E;T129W;F256R;N348H	++
923/924	K103E;T129W;N348H;S646D	++
871/872	W119Y;F254N;N348H;N457Q	++
933/934	K103E;W119Y;F254N;N348H;G444N	++
891/892	W119Y;F256R;N348H	++
929/930	F256R;N348H	++
841/842	K103E;W119Y;N348H	+
879/880	K103E;N348H;N494D	+
893/894	K103E;N348H;G444N	+
937/938	K103E;W119Y;T129W;G444N;N494D	+
941/942	K103E;F256R;G444N	+
915/916	K103E;W119Y;F254N;G444N	+
873/874	F254N;N457Q	+
899/900	K103E;N348H	+
901/902	K103E;W119Y;F254N;N348H	+
865/866	K103E;W119Y;N494D;S646D	+
867/868	K103E;F254N;N348H;N494D	+
949/950	N348H;G444N;S646D	+
917/918	W119Y;F256R;G444N	+
845/846	K103E;W119Y;F256R;N494D	+
885/886	K103E;F254N;N348H	+
927/928	W119Y;T129W;F254N;N348H;N494D	+
883/884	K103E;F254N;S646D	+
849/850	W119Y;N348H;N494D	+
861/862	W119Y;N348H	+
913/914	K103E;F256R;N494D	+
925/926	N348H;N494D	+
859/860	K103E;W119Y;N494D	+
951/952	W119Y;F256R	+
857/858	W119Y;N348H;G444N	+
921/922	K103E;T129W	+
875/876	K103E;G444N	+
931/932	K103E;F256R	+
947/948	K103E;N494D;S646D	+
843/844	N348H;G444N	+
853/854	K103E;N494D	+
847/848	K103E;W119Y	+
909/910	F256R;N494D	+
905/906	K103E;W119Y;T129W;F254N;F256R;N348H;N494D;S646D	+
919/920	K103E;F254N	+
869/870	W119Y;S646D	+
887/888	N348H	+
863/864	W119Y;G444N	+

[0231]

표 7.1 서열 번호: 300 대비 변이체의 활성

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 300 대비)	활성 FIOP [1] (서열 번호: 300 대비)
851/852	W119Y;T129W;S646D	+
907/908	K103E	+
889/890	K103E;F254N;F256R;N348H;G444N;N494D	+

[1] 활성 증가 수준은 서열 번호: 300의 참조 폴리펩티드 대비로 측정되었고,
이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가;
"++" = 2.0배 초과 3배 미만의 활성 증가; "+++" = 3배 초과 내지 10배 미만의 활성 증가;
"++++" = 10배 초과.

[0232]

[0233] **실시예 8**

[0234] **A1 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0235] **서열 번호: 1262 또는 1288 대비 개선**

[0236] 코덱스® 아실라제 패널(Codexis)로부터의 변이체, 및 미국 가특허 출원 제62/158,118호에 개시된 변이체에 대해 스크리닝한 결과, 위치 A1에서 A1/B1/B29 트리-페닐 아세테이트 인슐린으로부터 보호기를 제거하는 데 있어서 변이체 서열 번호: 1262 및 1288이 가장 우수한 효소인 것으로 확인되었다. 위치 A1에서의 삼중 보호된 인슐린의 탈아실화에 대한 개선된 활성 및 화학선택성을 표적화하는 라이브러리에 대한 모체 효소로서 서열 번호: 1262를 포함하는 변이체를 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다. 5 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 0.1 M 트리스-HCl 완충제 pH=8.0, 17 g/L 메틸 페닐 아세테이트 및 80 ㎕ 가용성 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 5시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론® 진탕기 중 100 rpm으로 인큐베이션시켰다. 반응물을 300 ㎕ 아세토니트릴로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 분석을 위해 HPLC에 적재하였다.

[0237] 서열 번호: 1262 또는 1288 대비 전환율(%)(전환율(%) FIOP)은 서열 번호: 1262 또는 1288에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 8.1 및 8.2에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

[0238] 서열 번호: 1262 또는 1288 대비 선택성(%)(선택성(%) FIOP)은 서열 번호: 1262 또는 1288에 의해 산출된 선택성(%) 대비 변이체에 의해 형성된 생성물의 선택성(%)으로서 계산되었고, 이는 표 8.1 및 8.2에 제시되어 있다. 선택성(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 8

표 8.1 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1262 대비)	탈아실화 전환율(%) FIOP [1]	탈아실화 선택성(%) FIOP [2]
953/954	W431R	+++	+++
955/956	F701L	+++++++	+++++++
957/958	F701A	+++++	+++++++
959/960	F24A	+++++	+++++++
961/962	F71V	+++	+++
963/964	F71K	+++	++++
965/966	F71E	+++++++	+++++++
967/968	F24Y;V28A	+++++	+++++
969/970	M697L	+++	+++
971/972	I177T	++++	++++
973/974	W154F;L754P	++	++
975/976	F71C;G74D	++	++
977/978	F701V	+++++++	+++++++
979/980	F701H	+++++++	+++++++
981/982	F701C	+++++	+++++++
983/984	F701I	+++++++	+++++++
985/986	F701M	++++	+++++
987/988	M697F	++	++
989/990	M697G	++++	++++
991/992	V28A;Y31F	+++++++	+++++++
993/994	V28A;Y31L	+++++++	+++++++
995/996	V28A;Y31V	+++++++	+++++++
997/998	V28A;Y31T	++++	++++
999/1000	V28A;Y31C	+++++	+++++++
1001/1002	V28A;Y31N	+++++++	+++++++
1003/1004	V28A;Y31M	+++++++	+++++++
1005/1006	V28A;Y31K	+++++++	+++++++
1007/1008	F24A;Y31W;V56I;F701W	+++++++	+++++++
1009/1010	F24A;V56I;F701W	+++++++	+++++++
1011/1012	F24A;Y31C;V56I;S386P;F701Y	++	+++++++
1013/1014	F24A;F71C;F701W	++++	+++++++
1015/1016	F24A;L225V;F701Y	+++	+++++++
1017/1018	F24A;Y31W;V56T;V264A;F701W;S750G	+++++++	+++++++
1019/1020	F24A;Y31W;F71C;F701W	+++	+++++++
1021/1022	F24A;D484N;F701W	+++++++	+++++++
1023/1024	F24A;V56T;F701W	+++++	+++++++
1025/1026	F24A;Y31W	+++++++	+++++++
1027/1028	F24A;V56I;W154F;I270V;M697L	+++	+++++++
1029/1030	F24A;V56I;M697F;F701W	+++	+++++++
1031/1032	F24A;Y31W;V56I;F701Y	++++	+++++++
1033/1034	F24A;Y31W;V56I;M697L	+++++++	+++++++

[0239]

표 8.1 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1262 대비)	탈아실화 전환율(%) FIOP [1]	탈아실화 선택성(%) FIOP [2]
1035/1036	F24Y;V28A;F71C;F701W	++++++	++++++
1037/1038	F24Y;V28A;V56I;A308T;T379A;F701W	++++++	++++++
1039/1040	F24Y;V28A;D321N;F701H	++++++	++++++
1041/1042	F24Y;V28A;N457Y;F701W	++++++	++++++
1043/1044	F24Y;V28A;V56I;F701W	++++++	++++++
1045/1046	F24Y;Y27C;V28T;F701W;V729F	++++++	++++++
1047/1048	V56T;F71G;F701W	++++++	++++++
1049/1050	M697L;F701Y	++++	++++
1051/1052	V56T;W658R;F701W	++	++
1053/1054	V56T;F71G;F701I	++++	++++++
1055/1056	A410P;M697F;F701W	+++++	++++++
1057/1058	V56L;K322R;M697L;F701V	+++++	++++++
1059/1060	V56L;F701H	++++++	++++++
1061/1062	Y31C;V56L;F701H	++++++	++++++
1063/1064	F71G;F701W	++++++	++++++
1065/1066	T129A;I511F;F701Y	++++	+++++
1067/1068	V56T;F701W;L711Q	++	++
1069/1070	I423T;F701W	++	++
1071/1072	V56I;W154F;F701W	+++	+++
1073/1074	V56L;W119R;K146E;F701Y	++++	++++++
1075/1076	V56T;M697L;F701W	++++++	++++++

[1] 각 변이체에 대한 전환율(%)은 서열 번호: 1262의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가; "++" = 2.0배 초과 3배 미만의 활성 증가; "+++" = 3배 초과 4배 미만의 활성 증가; "++++" = 4배 초과 5배 미만; "+++++" = 5배 초과 6배 미만; "++++++" = 6배 초과.

[2] 각 변이체에 대한 선택성(%)은 서열 번호: 1262의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 선택성 증가; "++" = 2.0배 초과 3배 미만의 선택성 증가; "+++" = 3배 초과 4배 미만의 선택성 증가; "++++" = 4배 초과 5배 미만의 선택성 증가; "+++++" = 5배 초과 6배 미만의 선택성 증가; "++++++" = 6배 초과의 선택성.

[0240]

표 8.2 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	탈아실화 전환율(%) FIOP[1]	탈아실화 선택성(%) FIOP[2]
1077/1078	G71Y;D74K	+++++	++++++
1079/1080	Y31A	+	+++
1081/1082	G71K;D74L	+	+++
1083/1084	G71K;D74N;T129P	+	+++
1085/1086	T32R	+	++++

[0241]

표 8.2 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	탈아실화 전환율(%) FIOP[1]	탈아실화 선택성(%) FIOP [2]
1087/1088	A69L;D74T	+	+++
1089/1090	V75H	+	++
1091/1092	R141A	+	+++
1093/1094	P22C	+	++++
1095/1096	F57W	+	++++
1097/1098	G71E	+	+++++
1099/1100	G71E;D74T	+++	++++
1101/1102	G71W;D74T	+++	++++
1103/1104	G71W;D74G	+++	++++
1105/1106	G71W;D74S	+++	++++
1107/1108	G71D;D74H	+++	++++
1109/1110	G71D;D74M	+++	++++
1111/1112	G71D;D74L	+++	++++
1113/1114	G71E;D74T;A470V	++	+++
1115/1116	G71W	++	++++
1117/1118	G71D	+++	++++
1119/1120	K394Y	++	++++
1121/1122	G71H;D74M	++	+++
1123/1124	G71I;D74Q;G145S	++	++
1125/1126	G71H;D74H	++	+++
1127/1128	F50W	+	++
1129/1130	G71I;A149V	+	++
1131/1132	G71N;D74Q	++	++
1133/1134	G71N;D74A	+	++
1135/1136	G71H	++	++
1137/1138	Y31L;V56I;V264A;A308T;T379A;D484N;Q547K;L711Q;S750G	+	++
1139/1140	G71N;D74V;Y248C	+	++
1141/1142	G71H;D74G	++	++
1143/1144	G71H;D74P	++	+++
1145/1146	G71N;D74S	++	++
1147/1148	G71F;D74E	++	++
1149/1150	G71Y;D74L	+++	+++
1151/1152	G71H;D74S	++	++
1153/1154	G71H;D74A	++	+++
1155/1156	G71L;D74M	+	+
1157/1158	G71T	++	++

[1] 각 변이체에 대한 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가; "++" = 2.0배 초과 3배 미만의 활성 증가; "+++" = 3배 초과 4배 미만의 활성 증가; "++++" = 4배 초과 5배 미만; "+++++" = 5배 초과 6배 미만; "++++++" = 6배 초과.

[2] 각 변이체에 대한 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 선택성 증가; "++" = 2.0배 초과 3배 미만의 선택성 증가; "+++" = 3배 초과 4배 미만의 선택성 증가; "++++" = 4배 초과 5배 미만의 선택성 증가; "+++++" = 5배 초과 6배 미만의 선택성 증가; "++++++" = 6배 초과의 선택성.

[0242]

[0243] **실시예 9**

[0244] **A1 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0245] **서열 번호: 1036 대비 개선**

[0246] 실시예 8에 기술된 변이체에 대해 스크리닝한 후, 서열 번호: 1036을 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0247] 5 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 200 mM 트리스 완충제 pH=8.0 및 10 ㎕ 가용성 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 5시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론® 진탕기 중 100 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴 또는 디메틸아세트아미드로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 물로 2배 희석시키고, 분석을 위해 HPLC에 적재하였다.

[0248] 서열 번호: 1036 대비 전환율(%)(전환율(%) FIOP)은 서열 번호: 1036에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 9.1에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

[0249] 서열 번호: 1036 대비 선택성(%)(선택성(%) FIOP)은 서열 번호: 1036에 의해 산출된 선택성(%) 대비 변이체에 의해 형성된 생성물의 선택성(%)으로서 계산되었고, 이는 표 9.1에 제시되어 있다. 선택성(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 9

표 9.1 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1036 대비)	탈아실화 전환율(%) FIOP [1]	탈아실화 선택성(%) FIOP [2]
1175/1176	A467L	+	+
1171/1172	T384Y	+	+
1177/1178	A255Y	+	+
1165/1166	D623E	+	+
1169/1170	L253M	+	+
1183/1184	T176C	+	+
1163/1164	A255S	+	+
1181/1182	T384R	+++	+
1159/1160	T384K	+	+
1185/1186	L536T	+	+
1189/1190	L536K	+	+
1193/1194	N2L	+++	+
1179/1180	F460Y	+	+
1167/1168	A255H	+	+
1187/1188	N47R	++	+
1161/1162	L253N	+++	
1173/1174	L253Q	+	
1191/1192	L536R	+	

[1] 전환율(%)은 서열 번호: 1036의 참조 폴리펩티드 대비로 측정되었고,
이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가;
"++" = 2.0배 초과 2.5배 미만의 활성 증가; "+++" = 2.5배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1036의 참조 폴리펩티드 대비로 측정되었고,
이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 선택성 증가;
"++" = 2.0배 초과 2.5배 미만의 선택성 증가; "+++" = 2.5배 초과의 선택성 증가.

[0250]

[0251] **실시예 10**

[0252] **A1 위치에서의 삼중 보호된 인슐린의 탈아실화에서**

[0253] **서열 번호: 1194 대비 개선**

[0254] 실시예 9에 기술된 변이체에 대해 스크리닝한 후, 서열 번호: 1194를 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0255] 15 g/L A1/B1/B29 트리-페닐 아세테이트 인슐린, 200 mM 트리스 완충제 pH=8.0 및 10 ㎕ 가용성 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 5시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론 중 100 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴 또는 디메틸아세트아미드로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 물로 2배 희석시키고, 분석을 위해 HPLC에 적재하였다.

[0256] 서열 번호: 1194 대비 전환율(%)(전환율(%) FIOP)은 서열 번호: 1194에 의해 산출된 전환율(%) 대비 변이체에

의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 10.1에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

[0257] 서열 번호: 1194 대비 선택성(%)(선택성(%) FIOP)은 서열 번호: 1194에 의해 산출된 선택성(%) 대비 변이체에 의해 형성된 생성물의 선택성(%)으로서 계산되었고, 이는 표 10.1에 제시되어 있다. 선택성(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 10

표 10.1 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1194 대비)	탈아실화 전환율(%) FIOP[1]	탈아실화 선택성(%) FIOP[2]
1195/1196	V264A;T384K;A467L;D484N;L536T;Q547K	+	+
1197/1198	V264A;T384R;A467L;D484N;L536T;Q547K	+	+
1199/1200	T384K;A467L;D484N;L536T;Q547K	+++	+
1201/1202	V264A;T384R;A467L;D484N;L536T;Q547K	+	+
1203/1204	V264A;T384R;A467L;D484N;L536T;Q547K	+	+
1205/1206	V264A;T384R;A467L;D484N;L536T;Q547K	+	+
1207/1208	T384R;A467L;D484N;L536T;Q547K	+++	
1209/1210	V264A;T384R;A467L;D484N;L536T;Q547K	+	+
1211/1212	A28T;V264A;T384R;A467L;D484N;L536T;Q547K	++	+
1213/1214	Q12A;K103E;W119Y;Q233K;T384R;G444N;N494D;S646D	++	
1215/1216	Q12A;K103E;T131A;Q233K;G444N;N494D;S646D	+	+
1217/1218	Q12A;K103E;W119Y;T131A;Q233K;G444N;N494D;S646D	+	+
1219/1220	Q12A;K103E;T131A;Q233K;G444N;A467L;N494D;S646D	++	+
1221/1222	Q12A;K103E;W119Y;Q233K;G444N;N494D;S646D	+	+
1223/1224	K103E;Q233K;G444N;N494D;S646D	+	+
1225/1226	Q12A;K103E;Q233K;G444N;N494D;S646D	+	
1227/1228	Q12A;K103E;W119Y;Q233K;G444N;N494D;S646D	+	+
1229/1230	K103E;W119Y;Q233K;G444N;N494D;S646D	+	+
1231/1232	Q12A;K103E;W119Y;T131A;Q233K;T384K;G444N;N494D;S646D	++	
1233/1234	Q12A;K103E;W119Y;Q233K;G444N;N494D;S646D	+	+
1235/1236	Q12A;K103E;W119Y;T131A;Q233K;G444N;N494D;S646D	+	+
1237/1238	Q12A;K103E;W119Y;T131A;Q233K;T384K;G444N;N	++	

[0258]

표 10.1 탈아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1194 대비)	탈아실화 전환율(%) FIOP[1]	탈아실화 선택성(%) FIOP[2]
	494D;S646D		
1239/1240	Q12A;K103E;W119Y;T131A;Q233K;G444N;N494D;S646D	+	+
1241/1242	Q12A;K103E;W119Y;T131A;Q233K;G444N;N494D;S646D	+	+
1243/1244	Q12A;K103E;W119Y;Q233K;G444N;A467L;N494D;S646D	+	+
1245/1246	Q12A;K103E;W119Y;Q233K;G444N;A467L;N494D;S646D	+	+
1247/1248	Q12A;K103E;W119Y;Q233K;G444N;N494D;L536T;S646D	+	+
1249/1250	K103E;W119Y;T131A;Q233K;T384R;G444N;N494D;S646D	++	
1251/1252	Q12A;W119Y;Q233K;T384R;G444N;N494D;S646D	+	+
1253/1254	K668E	+	+

[1] 전환율(%)은 서열 번호: 1194의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 활성 증가; "++" = 2.0배 초과 2.5배 미만의 활성 증가; "+++" = 2.5배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1194의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 1배 초과 2.0배 미만의 선택성 증가; "++" = 2.0배 초과 2.5배 미만의 선택성 증가; "+++" = 2.5배 초과의 선택성 증가.

[0259]

[0260] **실시예 11**

[0261] **A1, B1 및 B29 위치에서의 인슐린의 아실화에서의 개선**

[0262] 코덱스® 아실라제 패널(Codexis) 중의, 및 미국 가특허 출원 제62/158,118호에 개시된 변이체로 이루어진 선택된 변이체들을 A1, B1, 및 B29 위치에서 인슐린을 아실화시킬 수 있는 그의 능력에 대해 스크리닝하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0263] 10 g/L 인슐린, 0.1 M CHES 완충제 pH=10, 17 g/L 메틸 페닐아세테이트 및 20 ㎕ 가용성 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 20시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론® 진탕기 중 300 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 분석을 위해 HPLC에 적재하였다.

[0264] 전환율(%)(전환율(%))은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다. 선택성(%)(선택성(%))은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다. 결과는 도 2a 내지 도 2h에 제시되어 있다.

[0265] **실시예 12**

[0266] **A1, B1 및 B29 위치에서의 인슐린의 아실화에서**

[0267] **서열 번호: 1288 대비 개선**

[0268] 실시예 11에 기술된 변이체에 대해 스크리닝하고, 위치 B29에서 인슐린을 아실화시키는 데 있어서 가장 우수한 효소인 것으로 확인한 후, 서열 번호: 1288을 모체 효소로서 선택하였다. 잘 확립된 기술(예컨대, 포화 돌연변이유발법, 앞서 확인된 유익한 돌연변이의 재조합)을 사용하여 조작된 유전자로 이루어진 라이브러리를 제조하였다. 실시예 2에 기술된 바와 같이 HTP에서 각 유전자에 의해 코딩되는 폴리펩티드를 제조하고, 실시예 3에 기술된 바와 같이 가용성 용해물을 생성하였다.

[0269] 10 g/L 인슐린, 0.1 M TRIS 완충제 pH=9.25, 20% 아세토니트릴, 17 g/L 메틸 페닐아세테이트 및 10 ㎕ 정화된 용해물로 구성된 200 ㎕ 반응물 중에서 각 변이체를 30℃에서 5시간 동안 스크리닝하였다. 96 웰 플레이트를 가열 밀봉하고, 써모트론® 진탕기 중 100 rpm으로 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 분석을 위해 HPLC에 적재하였다.

[0270] 서열 번호: 1288 대비 전환율(%)(전환율(%) FIOP)은 서열 번호: 1288에 의해 산출된 전환율(%) 대비 변이체에 의해 형성된 생성물의 전환율(%)로서 계산되었고, 이는 표 12.1, 12, 2, 12,3, 12.4, 12.5, 12.6, 및 12.7에 제시되어 있다. 전환율(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 기질, 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

[0271] 서열 번호: 1288 대비 선택성(%)(선택성(%) FIOP)은 서열 번호: 1288에 의해 산출된 선택성(%) 대비 변이체에 의해 형성된 생성물의 선택성(%)으로서 계산되었고, 이는 표 12.1, 12, 2, 12,3, 12.4, 12.5, 12.6, 및 12.7에 제시되어 있다. 선택성(%)은 HPLC 분석에 의해 관찰된 바와 같은, 생성물 피크 면적을 생성물, 및 불순물/부산물 피크 면적의 총합으로 나눔으로써 계산되었다.

표 12

[0272]

표 12.1 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1 아실화 전환율(%) (FIOP)[1]	A1 아실화 선택성(%) (FIOP)[2]
1677/1678	Y27T;F254W;A470V	++	+
1679/1680	Y27T;L253V;A255G;N348R	+	+
1685/1686	Y27T;A255G;W370I	+++	
1701/1702	Y27T;D74S;F254W;A255G;N348R;K369C;T384P	+	+
1703/1704	Y27T;D74N;L253V;F254W;N348R;K369C;T384P	++	+
1759/1760	L253M	+	+
1797/1798	T384R	++	+
1799/1800	D623N	+	
1811/1812	L253S	+	+
1817/1818	N457T	+	+
1819/1820	R317S;Q380P	+	+
1821/1822	A373Y	+	+
1859/1860	K128W	+	+
1901/1902	T705S	+	+

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 1배 초과 1.5배 미만의 활성 증가; "++" = 1.5배 초과 2.0배 미만의 활성 증가;
"+++" = 2.0배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 0.95배 초과의 선택성 증가.

[0273]

표 12.2 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B29 아실화 전환율(%) (FIOP)[1]	B29 아실화 선택성(%) (FIOP)[2]
1371/1372	Y27T;N348R;D381K	+	+
1417/1418	Y27T;D74S;A255G;N348R;K369C;D381K		+
1605/1606	Y27T;D74S;A255G;N348R;D381K;T384P	+	+
1637/1638	Y27T;N348R;K369C;W370I;D381K;T384P		+
1659/1660	Y27T;D74G;F254W;A255G;N348R;K369C;W370I;D381K		+
1689/1690	Y27T;F254W;A255G;N348R;W370I;D381K		+
1707/1708	Y27T;A255G;N348R;W370I;D381K;T384P		+
1711/1712	D381F	+	+
1715/1716	Q134M	+	+
1717/1718	D623W	++	+
1719/1720	L253R	+	+

표 12.2 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B29 아실화 전환율(%) (FIOP)[1]	B29 아실화 선택성(%) (FIOP)[2]
1721/1722	N627M	+	+
1723/1724	N627R	+	+
1725/1726	D623N	++	+
1729/1730	K615V	+	+
1731/1732	D381L	+	+
1733/1734	D381R	+	++
1735/1736	A132G	+	+
1737/1738	A467S	+	+
1741/1742	F256Y	+	+
1743/1744	D623V	+	+
1745/1746	K615H		+
1747/1748	D623A	+	+
1749/1750	D381Q	+	+
1753/1754	K615C		+
1755/1756	T384R	+	+
1761/1762	F256H	+	+
1773/1774	T453C		+
1775/1776	D381V		+
1777/1778	D381K	+	+
1779/1780	D381F;Q672K		+
1781/1782	D623Y	+	+
1785/1786	D623R	+++	++
1787/1788	D623F	+	+
1789/1790	D623K	+++	++
1793/1794	D381I		+
1823/1824	A373K	+++	++
1825/1826	S706K	+	++
1829/1830	N348K;A467T	+	+
1831/1832	D709G	+	+
1833/1834	D709A	+	+
1835/1836	F620R	+	+
1837/1838	D709N	+	++
1841/1842	D709H	+	+
1843/1844	E377A		+
1845/1846	F620K	+	+
1847/1848	S706R		+
1849/1850	D709R	+	++++
1853/1854	N20S;D709Q		+
1857/1858	D709S	+	+
1867/1868	V618C	+	+
1871/1872	A69M		+
1875/1876	F254K	+	+
1877/1878	A84V		+
1879/1880	F701H		+
1881/1882	P383K		+
1883/1884	A69L		+++
1885/1886	I708V		+

[0274]

표 12.2 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B29 아실화 전환율(%) (FIOP)[1]	B29 아실화 선택성(%) (FIOP)[2]
1889/1890	A255K	++	++
1893/1894	A255R	++	++
1895/1896	A69V		+
1897/1898	P383R		++++

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 4배 미만의 활성 증가; "++" = 4배 초과 6배 미만의 활성 증가;
"+++" = 6배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2.0배 초과 5배 미만의 선택성 증가; "++" = 5.0배 초과 10배 미만의 선택성 증가;
"+++" = 10.0배 초과 15배 미만의 선택성 증가; "++++" = 15.0배 초과의 선택성.

[0275]

표 12.3 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1 아실화 전환율(%) (FIOPC)[1]	B1 아실화 선택성(%) (FIOPC)[2]
1315/1316	Y27T;L253V	+	
1317/1318	Y27T;D74G;L253V;F254W	++	+
1323/1324	Y27T;D74G;L253V;A255G;N348R;W370I;T384P	++	+
1325/1326	Y27T;D74N;L253V;F254W;N348R;W370I;D381K;T384P	++	++
1327/1328	Y27T;D74N;L253V;F254W;A255G;N348R;W370I	++	++
1335/1336	Y27T;D74G;L253V;N348R;K369C;W370I;D381F;T384P	+	+
1337/1338	Y27T;L253V;F254W;N348R	+	
1339/1340	Y27T;D74P;L253V;F254W;A255G;N348R	+	+
1345/1346	Y27T;D74G;L253V;F254W;A255G;W370I	++	++
1347/1348	Y27T;L253V;F254W;A255G	+	
1349/1350	Y27T;D74G;L253V;F254W;T384P	++	+
1351/1352	Y27T;D74N;F254W;N348R;W370I	+	+
1353/1354	Y27T;D74S;L253V;N348R;W370I;D381K;T384P	++	+
1357/1358	Y27T;L253V;A255G;W370I	+	+
1359/1360	Y27T;D74G;F254W;A255G;D381F	+	+
1365/1366	Y27T;L253V;K369C;W370I	+	

[0276]

표 12.3 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1 아실화 전환율(%) (FIOPC)[1]	B1 아실화 선택성(%) (FIOPC)[2]
1377/1378	Y27T;L253V;F254W;N348R;D381F	+	+
1379/1380	Y27T;L253V;F254W;A255G;N348R;W370I	+	+
1381/1382	Y27T;D74S;L253V;A255G;T384P	+	+
1387/1388	Y27T;D74N;L253V;N348R;W370I;D381W;T384P	++	+
1393/1394	Y27T;D74P;L253V;N348R	+	+
1399/1400	Y27T;D74G;F254W;A255G;N348R;K369C;W370I;D381F	+	+
1401/1402	Y27T;D74P;F254W;A255G;N348R;K369C;W370I	+	+
1403/1404	Y27T;D74N;L253V;F254W;W370I;D381K	++	++
1409/1410	Y27T;D74G;L253V;T384P	+	+
1411/1412	Y27T;D74S;N348R;W370I	+	+
1413/1414	Y27T;D74S;L253V;F254W;A255G;K369C;W370I	+	+
1419/1420	Y27T;D74G;L253V;N348R;K369C;W370I	+	
1425/1426	Y27T;D74N;L253V;F254W;A255G	++	+
1429/1430	Y27T;D74P;L253V;F254W;N348R	+	+
1435/1436	Y27T;D74G;A255G;W370I	+	+
1437/1438	Y27T;D74G;L253V;A255G;N348R;D381W	+	+
1439/1440	Y27T;D74P;L253V;W370I	++	+
1441/1442	Y27T;L253V;N348R;W370I;T384P	+	
1443/1444	Y27T;D74G;L253V;F254W;A255G;W370I;D381K;T384P	++	+
1447/1448	Y27T;D74N;F254W;A255G;N348R;W370I;D381K	+	+
1449/1450	Y27T;D74S;L253V;N348R;K369C;W370I;T384P	+	+
1453/1454	Y27T;D74N;L253V;F254W;N348R;W370I;D381F	++	++
1455/1456	Y27T;D74S;F254W;A255G;N348R;W370I;D381F;T384P	+	+
1457/1458	Y27T;D74G;L253V;F254W;A255G;D381K	++	++
1459/1460	Y27T;D74S;F254W;K369L;W370I	+	+
1463/1464	Y27T;L253V;F254W;D381F;T384P	+	+
1465/1466	Y27T;D74G;L253V;F254W;A255G;K369C;W370I	+	
1467/1468	Y27T;D74G;F254W;A255G;N348R;W370I	++	+
1469/1470	Y27T;D74G;L253V;F254W;A255G;N348R;W370I;T384P	++	++
1471/1472	L253V;N348R;W370I	+	

[0277]

[0278]

표 12.3 아실화 결과			
서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1 아실화 전환율(%) (FIOPC)[1]	B1 아실화 선택성(%) (FIOPC)[2]
1475/1476	Y27T;D74N;L253V;F254W;K369C	+	+
1477/1478	Y27T;D74G;F254W;A255G;N348R	+	
1479/1480	Y27T;D74S;L253V;N348R;D381W	+	+
1481/1482	Y27T;D74S;L253V;N348R	+	+
1483/1484	Y27T;L253V;F254W;A255G;N348R	+	
1489/1490	Y27T;D74S;L253V;A255G;N348R;W370I;D381K	++	++
1491/1492	Y27T;F254W;A255G;N348R;K369C;W370I	+	+
1493/1494	Y27T;D74N;L253V;F254W;A255G;N348R;W370I;T384P	++	+++
1495/1496	Y27T;D74S;F254W;A255G;W370I	++	++
1497/1498	Y27T;F254W;A255G;K369C;W370I;D381F;T384P	+	
1501/1502	Y27T;L253V;F254W;D381F	++	+
1503/1504	Y27T;D74N;F254W;N348R	+	
1505/1506	Y27T;F254W;A255G;W370I	+	
1509/1510	Y27T;D74N;A107V;A255G;N348R;K369C;W370I	+	
1511/1512	Y27T;F254W;A255G;N348R;W370I	+	
1515/1516	Y27T;D74N;F254W	+	+
1521/1522	Y27T;D74G;L253V;D381F;T384P	+	+
1523/1524	Y27T;D74P;L253V;A255G	+	+
1525/1526	Y27T;D74S;L253V;F254W;A255G;N348R	+	+
1529/1530	Y27T;D74S;F254W;A255G;N348R;K369C;W370I	+	
1533/1534	Y27T;D74P;W370I	+	
1537/1538	Y27T;L253V;F254W;T384P	+	+
1543/1544	Y27T;D74N;L253V;F254W;A255G;W370I	+++	+++
1545/1546	Y27T;D74G;L253V;N348R;W370I	++	+
1553/1554	Y27T;F254W;A255G;N348R;W370I;T384P	+	
1555/1556	Y27T;D74G;L253V;F254W;N348R	+	+
1563/1564	Y27T;L253V;A255G;W370I;D381F;T384P	+	
1565/1566	Y27T;L253V;A255G;N348R;D381K	+	+
1567/1568	Y27T;L253V;F254W;N348R;W370I;T384P	+	+
1569/1570	Y27T;D74N;F254W;N348R;W370I;D381K	+	+
1571/1572	Y27T;D74N;L253V;A255G;N348R;K369C;W370I	+	+
1573/1574	Y27T;L253V;F254W;N348R;D381W;T384P	+	+
1577/1578	Y27T;L253V;F254W;A255G;G260C	+	+

표 12.3 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1 아실화 전환율(%) (FIOPC)[1]	B1 아실화 선택성(%) (FIOPC)[2]
	;N348R;D381F;T384P		
1579/1580	Y27T;D74P;L253V;F254W;N348R; D381F;T384P	+	+
1583/1584	Y27T;D74G;L253V;N348R;K369C; W370I;D381F	+	+
1585/1586	Y27T;D74N;L253V;N348R	+	+
1587/1588	Y27T;D74G;L253V;A255G;N348R; T384P	+	+
1589/1590	Y27T;D74N;L253V;A255G;W370I	++	++
1591/1592	Y27T;D74N;A255G;N348R;W370I	+	+
1593/1594	Y27T;L253V;N348R;D381F;T384P	+	
1603/1604	Y27T;L253V;D381F;T384P	+	
1607/1608	Y27T;D74P;L253V;F254W;N348R; W370I;D381W;T384P	++	+
1609/1610	Y27T;L253V;F254W;A255G;N348R ;W370I;T384P	+	
1627/1628	Y27T;L253V;F254W	+	+
1631/1632	Y27T;L253V;F254W;N348R;W370I; D381F	++	++
1633/1634	Y27T;D74G;L253V;A255G	+	+
1635/1636	Y27T;D74N;L253V;F254W;N348R; W370I	+++	+++
1639/1640	Y27T;D74N;L253V;F254W;N348R; K369C;W370I;D381K	+	+
1643/1644	Y27T;D74G;L253V;F254W;A255G; N348R;K369C;W370I;D381F	+	+
1645/1646	Y27T;D74G;L253V;F254W;N348R; K369C;W370I	+	+
1655/1656	Y27T;D74N;L253V	+	+
1657/1658	Y27T;D74G;L253V;F254W;A255G; N348R	+	+
1661/1662	Y27T;F254W;A255G;T384P	+	
1663/1664	Y27T;F254W;A255G	++	+
1667/1668	Y27T;L253V;F254W;A255G;N348R ;D381F;T384P	+	+
1669/1670	Y27T;F254W;A255G;N348R	+	+
1671/1672	Y27T;D74N;F254W;T384P	+	
1673/1674	Y27T;L253V;N348R	+	+
1675/1676	Y27T;D74G;A255G;N348R	+	
1677/1678	Y27T;F254W;A470V	+	
1679/1680	Y27T;L253V;A255G;N348R	+	
1681/1682	Y27T;D74N;L253V;K369C;D381K; T384P	+	+
1683/1684	Y27T;D74G;L253V;A255G;N348R; D381F	++	+
1685/1686	Y27T;A255G;W370I	+	
1687/1688	Y27T;D74S;F254W;A255G;N348R	+	

[0279]

표 12.3 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1 아실화 전환율(%) (FIOPC)[1]	B1 아실화 선택성(%) (FIOPC)[2]
1693/1694	Y27T;D74S;L253V;F254W;N348R;D381W;T384P	+++	++
1695/1696	Y27T;D74N;F254W;A255G;N348R	+	
1697/1698	Y27T;D74P;L253V;F254W;A255G	++	+
1705/1706	Y27T;L253V;N348R;W370I;D381F;T384P	++	++
1709/1710	Y27T;D74S;A255G;W370I	+	
1815/1816	N388E	+	++
1865/1866	A255P	+	

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 5배 미만의 활성 증가; "++" = 5배 초과 10배 미만의 활성 증가;
"+++" = 10배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2.0배 초과 5배 미만의 선택성 증가; "++" = 5.0배 초과 7배 미만의 선택성 증가;
"+++" = 7.0배 초과의 선택성.

[0280]

표 12.4 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B29 아실화 선택성(%) (FIOPC)[2]
1319/1320	Y27T;D74S;F254W;N348R;D381W	+	+
1329/1330	Y27T;A255G;N348R;W370I	+	
1333/1334	Y27T;N348R;T384P	+	+
1363/1364	Y27T;D74G;F254W;A255G;N348R;D381W	+	+
1373/1374	Y27T;D74S;N348R	+	
1499/1500	Y27T;A255G;N348R	+	+
1507/1508	Y27T;L253V;N348R;D381F;T384P	+	+
1541/1542	Y27T;L253V;F254W;N348R;T384P	+	
1551/1552	Y27T;D74P;F254W;A255G;N348R;D381K;T384P	+	+
1595/1596	Y27T;N348R	+	+
1599/1600	Y27T;F254W;A255G;N348R;W370I;D381W;T384P	+	
1605/1606	Y27T;D74S;A255G;N348R;D381K;T384P	+	+
1613/1614	Y27T;D74G;F254W;N348R;D381W;T384P	+	+
1615/1616	Y27T;F254W;A255G;D381K;T384P	+	+

[0281]

표 12.4 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B29 아실화 선택성(%) (FIOPC)[2]
1621/1622	Y27T;D74S;F254W;N348R;D381F	+	+
1647/1648	Y27T;A255G;N348R;D381W;T384P	+	+
1651/1652	Y27T;F254W;N348R;D381W;T384P	+	+
1653/1654	Y27T;D74G;N348R	+	+
1661/1662	Y27T;F254W;A255G;T384P	++	+
1663/1664	Y27T;F254W;A255G	++	+
1665/1666	Y27T;D74S;L253V;N348R	+++	++
1667/1668	Y27T;L253V;F254W;A255G;N348R;D381F;T384P	+	+
1669/1670	Y27T;F254W;A255G;N348R	+	+
1671/1672	Y27T;D74N;F254W;T384P	+++	+
1673/1674	Y27T;L253V;N348R	+	
1675/1676	Y27T;D74G;A255G;N348R	++	++
1677/1678	Y27T;F254W;A470V	+	
1679/1680	Y27T;L253V;A255G;N348R	+	+
1683/1684	Y27T;D74G;L253V;A255G;N348R;D381F	++	+
1685/1686	Y27T;A255G;W370I	++	+
1687/1688	Y27T;D74S;F254W;A255G;N348R	+++	++
1691/1692	Y27T;D74N;L253V;F254W	+	
1693/1694	Y27T;D74S;L253V;F254W;N348R;D381W;T384P	++	++
1695/1696	Y27T;D74N;F254W;A255G;N348R	+++	++
1699/1700	Y27T;D74G;L253V;F254W;A255G;N348R	+++	+
1705/1706	Y27T;L253V;N348R;W370I;D381F;T384P	+	+
1707/1708	Y27T;A255G;N348R;W370I;D381K;T384P	+	+
1709/1710	Y27T;D74S;A255G;W370I	++	+
1717/1718	D623W	+	+
1719/1720	L253R	+	+
1747/1748	D623A	+	+
1757/1758	D623N	+	+
1761/1762	F256H	+	+
1763/1764	A616R	+	
1771/1772	D623L	+	+
1781/1782	D623Y	+	+
1787/1788	D623F	+	+
1789/1790	D623K	+	+
1803/1804	D381Q	+	+
1805/1806	T384R	++	++
1813/1814	D623R	++	+++
1823/1824	A373K	+	++
1851/1852	H472R	+	
1855/1856	F620R	+	+
1865/1866	A255P	+	

[0282]

표 12.4 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B29 아실화 선택성(%) (FIOPC)[2]
1875/1876	F254K	+	+
1893/1894	A255R	+	+

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 5배 미만의 활성 증가; "++" = 5배 초과 10배 미만의 활성 증가;
"+++" = 10배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2.0배 초과 5배 미만의 선택성 증가; "++" = 5.0배 초과 7배 미만의 선택성 증가;
"+++" = 7.0배 초과의 선택성.

[0283]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
1313/1314	Y27T;L253V;A255G;N348R;T384P	+	+
1315/1316	Y27T;L253V	+	+
1317/1318	Y27T;D74G;L253V;F254W	+	+
1323/1324	Y27T;D74G;L253V;A255G;N348R;W370I;T384P	+	+
1325/1326	Y27T;D74N;L253V;F254W;N348R;W370I;D381K;T384P	+	+
1327/1328	Y27T;D74N;L253V;F254W;A255G;N348R;W370I	+	+
1329/1330	Y27T;A255G;N348R;W370I	+	+
1331/1332	Y27T;D74P;L253V;F254W;A255G;N348R;K369C;W370I	+	+
1335/1336	Y27T;D74G;L253V;N348R;K369C;W370I;D381F;T384P	+	+
1337/1338	Y27T;L253V;F254W;N348R	+	+
1339/1340	Y27T;D74P;L253V;F254W;A255G;N348R	+	+
1341/1342	Y27T	+	
1343/1344	Y27T;D74G;L253V;N348R;K369C;W370I	+	+
1345/1346	Y27T;D74G;L253V;F254W;A255G;W370I	++	+
1347/1348	Y27T;L253V;F254W;A255G	+	+
1349/1350	Y27T;D74G;L253V;F254W;T384P	+	+

[0284]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
1351/1352	Y27T;D74N;F254W;N348R;W370I	+	+
1353/1354	Y27T;D74S;L253V;N348R;W370I;D381K;T384P	+	+
1357/1358	Y27T;L253V;A255G;W370I	+	+
1359/1360	Y27T;D74G;F254W;A255G;D381F	+	+
1365/1366	Y27T;L253V;K369C;W370I	+	+
1375/1376	Y27T;D74P;F254W;A255G;N348R	+	+
1377/1378	Y27T;L253V;F254W;N348R;D381F	+	+
1381/1382	Y27T;D74S;L253V;A255G;T384P	+	+
1383/1384	Y27T;D74G;A255G;W370I	+	+
1385/1386	Y27T;D74S;N348R	+	
1387/1388	Y27T;D74N;L253V;N348R;W370I;D381W;T384P	+	+
1389/1390	Y27T;D74G;L253V;F254W;N348R	+	+
1393/1394	Y27T;D74P;L253V;N348R	+	+
1395/1396	Y27T;L253V;F254W;A255G;N348R	+	+
1397/1398	Y27T;D74S;L253V;F254W;A255G;N348R	+	+
1399/1400	Y27T;D74G;F254W;A255G;N348R;K369C;W370I;D381F	+	+
1401/1402	Y27T;D74P;F254W;A255G;N348R;K369C;W370I	+	+
1403/1404	Y27T;D74N;L253V;F254W;W370I;D381K	++	+
1405/1406	Y27T;D74G;F254W;K369C;W370I	+	+
1407/1408	Y27T;D74G;L253V;N348R;W370I	+	+
1409/1410	Y27T;D74G;L253V;T384P	+	+
1411/1412	Y27T;D74S;N348R;W370I	+	+
1413/1414	Y27T;D74S;L253V;F254W;A255G;K369C;W370I	+	+
1421/1422	Y27T;D74G;F254W;A255G;N348R	+	+
1423/1424	Y27T;L253V;N348R;W370I;T384P	+	+
1425/1426	Y27T;D74N;L253V;F254W;A255G	+	+
1427/1428	Y27T;L253V;F254W	+	+
1431/1432	Y27T;D74G;K369C;W370I	+	+
1433/1434	Y27T;F254W;A449V	+	+
1437/1438	Y27T;D74G;L253V;A255G;N348R;D381W	+	+
1439/1440	Y27T;D74P;L253V;W370I	+	+
1443/1444	Y27T;D74G;L253V;F254W;A255G;W370I;D381K;T384P	++	+
1447/1448	Y27T;D74N;F254W;A255G;N348R;W370I;D381K	+	+
1449/1450	Y27T;D74S;L253V;N348R;K369C;W370I;T384P	+	+
1451/1452	Y27T;D74N;L253V;N348R	+	+
1453/1454	Y27T;D74N;L253V;F254W;N348R;W	+	+

[0285]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
	370I;D381F		
1455/1456	Y27T;D74S;F254W;A255G;N348R;W370I;D381F;T384P	+	+
1457/1458	Y27T;D74G;L253V;F254W;A255G;D381K	+	+
1459/1460	Y27T;D74S;F254W;K369L;W370I	+	+
1463/1464	Y27T;L253V;F254W;D381F;T384P	+	+
1465/1466	Y27T;D74G;L253V;F254W;A255G;K369C;W370I	+	+
1467/1468	Y27T;D74G;F254W;A255G;N348R;W370I	+	+
1469/1470	Y27T;D74G;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1471/1472	L253V;N348R;W370I	+	+
1473/1474	Y27T;F254W;N348R;W370I	+	+
1475/1476	Y27T;D74N;L253V;F254W;K369C	+	+
1479/1480	Y27T;D74S;L253V;N348R;D381W	+	+
1485/1486	Y27T;D74S;A255G	+	+
1489/1490	Y27T;D74S;L253V;A255G;N348R;W370I;D381K	+	+
1493/1494	Y27T;D74N;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1495/1496	Y27T;D74S;F254W;A255G;W370I	++	+
1497/1498	Y27T;F254W;A255G;K369C;W370I;D381F;T384P	+	+
1501/1502	Y27T;L253V;F254W;D381F	+	+
1503/1504	Y27T;D74N;F254W;N348R	+	+
1505/1506	Y27T;F254W;A255G;W370I	++	+
1509/1510	Y27T;D74N;A107V;A255G;N348R;K369C;W370I	+	+
1511/1512	Y27T;F254W;A255G;N348R;W370I	+	+
1515/1516	Y27T;D74N;F254W	+	+
1517/1518	Y27T;D74S;F254W;K369C;T384P	+	+
1521/1522	Y27T;D74G;L253V;D381F;T384P	+	+
1523/1524	Y27T;D74P;L253V;A255G	+	+
1527/1528	Y27T;D74G;A255G;N348R;K369C;W370I	+	+
1529/1530	Y27T;D74S;F254W;A255G;N348R;K369C;W370I	+	+
1531/1532	Y27T;F254W;A255G;N348R;K369C;W370I	+	+
1533/1534	Y27T;D74P;W370I	+	+
1535/1536	Y27T;D74P;L253V;F254W;N348R;K369C;W370I	+	+
1537/1538	Y27T;L253V;F254W;T384P	+	+
1541/1542	Y27T;L253V;F254W;N348R;T384P	+	+
1543/1544	Y27T;D74N;L253V;F254W;A255G;W	+	+

[0286]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
	370I		
1547/1548	Y27T;F254W;A255G;N348R	+	+
1549/1550	Y27T;D74S;F254W;N348R	+	+
1553/1554	Y27T;F254W;A255G;N348R;W370I;T384P	+	+
1557/1558	D74N;L253V;F254W;K369C;W370I	+	+
1561/1562	Y27T;D74S;K369C;W370I;D381K;T384P	+	+
1563/1564	Y27T;L253V;A255G;W370I;D381F;T384P	++	+
1567/1568	Y27T;L253V;F254W;N348R;W370I;T384P	+	+
1569/1570	Y27T;D74N;F254W;N348R;W370I;D381K	+	+
1571/1572	Y27T;D74N;L253V;A255G;N348R;K369C;W370I	+	+
1573/1574	Y27T;L253V;F254W;N348R;D381W;T384P	+	+
1577/1578	Y27T;L253V;F254W;A255G;G260C;N348R;D381F;T384P	+	
1579/1580	Y27T;D74P;L253V;F254W;N348R;D381F;T384P	+	+
1587/1588	Y27T;D74G;L253V;A255G;N348R;T384P	+	+
1589/1590	Y27T;D74N;L253V;A255G;W370I	+	+
1591/1592	Y27T;D74N;A255G;N348R;W370I	+	+
1599/1600	Y27T;F254W;A255G;N348R;W370I;D381W;T384P	+	+
1601/1602	Y27T;L253V;A255G;N348R;K369C;W370I	+	+
1603/1604	Y27T;L253V;D381F;T384P	+	+
1607/1608	Y27T;D74P;L253V;F254W;N348R;W370I;D381W;T384P	+	+
1609/1610	Y27T;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1611/1612	A255G;N348R;W370I	+	+
1613/1614	Y27T;D74G;F254W;N348R;D381W;T384P	+	
1615/1616	Y27T;F254W;A255G;D381K;T384P	+	+
1623/1624	Y27T;D74N;F254W;A255G;K369C	+	+
1625/1626	Y27T;D74P;L253V;F254W;N348R	+	+
1631/1632	Y27T;L253V;F254W;N348R;W370I;D381F	+	+
1633/1634	Y27T;D74G;L253V;A255G	+	+
1635/1636	Y27T;D74N;L253V;F254W;N348R;W370I	+	+
1643/1644	Y27T;D74G;L253V;F254W;A255G;N348R;K369C;W370I;D381F	+	+

[0287]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
1645/1646	Y27T;D74G;L253V;F254W;N348R;K369C;W370I	+	+
1649/1650	Y27T;L253V;F254W;A255G;N348R;W370I	++	+
1655/1656	Y27T;D74N;L253V	+	+
1661/1662	Y27T;F254W;A255G;T384P	++	++
1663/1664	Y27T;F254W;A255G	++	++
1665/1666	Y27T;D74S;L253V;N348R	++	++
1667/1668	Y27T;L253V;F254W;A255G;N348R;D381F;T384P	+	+
1671/1672	Y27T;D74N;F254W;T384P	+++	++
1673/1674	Y27T;L253V;N348R	+	+
1675/1676	Y27T;D74G;A255G;N348R	+	+
1677/1678	Y27T;F254W;A470V	+	+
1679/1680	Y27T;L253V;A255G;N348R	+	+
1683/1684	Y27T;D74G;L253V;A255G;N348R;D381F	+	+
1685/1686	Y27T;A255G;W370I	++	++
1687/1688	Y27T;D74S;F254W;A255G;N348R	++	+
1691/1692	Y27T;D74N;L253V;F254W	++++	++
1693/1694	Y27T;D74S;L253V;F254W;N348R;D381W;T384P	++	++
1695/1696	Y27T;D74N;F254W;A255G;N348R	++	+
1697/1698	Y27T;D74P;L253V;F254W;A255G	+++	++
1699/1700	Y27T;D74G;L253V;F254W;A255G;N348R	++	++
1701/1702	Y27T;D74S;F254W;A255G;N348R;K369C;T384P	+	
1703/1704	Y27T;D74N;L253V;F254W;N348R;K369C;T384P	+	+
1705/1706	Y27T;L253V;N348R;W370I;D381F;T384P	+	+
1709/1710	Y27T;D74S;A255G;W370I	+++	++
1711/1712	D381F	+	+
1713/1714	A132S	+	+
1715/1716	Q134M	+	+
1717/1718	D623W	+	+
1727/1728	T131L	+	+
1731/1732	D381L	+	+
1735/1736	A132G	+	+
1751/1752	W370V	+	+
1765/1766	D381R	+	+
1769/1770	T384R	+	+
1791/1792	D623Y	+	+
1799/1800	D623N	+	+
1801/1802	D623R	+	+
1807/1808	S619I	+	

[0288]

표 12.5 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1 아실화 전환율(%) (FIOPC)[1]	A1/B1 아실화 선택성(%) (FIOPC)[2]
1809/1810	L253V	+	+
1839/1840	T133K	+	
1865/1866	A255P	+	+
1887/1888	I708M	+	
1891/1892	F254T	+	+
1899/1900	T705S	+	

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 10배 미만의 활성 증가; "++" = 10배 초과 50배 미만의 활성 증가;
"+++" = 50배 초과 100배 미만의 활성 증가; "++++" = 100배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 10배 미만의 선택성 증가; "++" = 10배 초과 50배 미만의 선택성 증가;
"+++" = 50배 초과 100배 미만의 선택성 증가; "++++" = 100배 초과의 선택성 증가.

[0289]

[0290]

표 12.6 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1/B29 아실화 전환율(%) (FIOPC)[1]	B1/B29 아실화 선택성(%) (FIOPC)[2]
1323/1324	Y27T;D74G;L253V;A255G;N348R;W370I;T384P	+	+
1325/1326	Y27T;D74N;L253V;F254W;N348R;W370I;D381K;T384P	+	+
1327/1328	Y27T;D74N;L253V;F254W;A255G;N348R;W370I	+	+
1345/1346	Y27T;D74G;L253V;F254W;A255G;W370I	+	
1349/1350	Y27T;D74G;L253V;F254W;T384P	+	
1353/1354	Y27T;D74S;L253V;N348R;W370I;D381K;T384P	+	+
1387/1388	Y27T;D74N;L253V;N348R;W370I;D381W;T384P	++	+
1389/1390	Y27T;D74G;L253V;F254W;N348R	+	
1391/1392	Y27T;L253V;F254W;A255G;N348R;K369C;W370I;D381W;T384P	+	+
1397/1398	Y27T;D74S;L253V;F254W;A255G;N348R	+	+
1403/1404	Y27T;D74N;L253V;F254W;W370I;D381K	+	+

표 12.6 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1/B29 아실화 전환율(%) (FIOPC)[1]	B1/B29 아실화 선택성(%) (FIOPC)[2]
1411/1412	Y27T;D74S;N348R;W370I	+	+
1425/1426	Y27T;D74N;L253V;F254W;A255G	+	
1435/1436	Y27T;D74G;A255G;W370I	+	+
1437/1438	Y27T;D74G;L253V;A255G;N348R;D381W	+	+
1439/1440	Y27T;D74P;L253V;W370I	+	+
1443/1444	Y27T;D74G;L253V;F254W;A255G;W370I;D381K;T384P	++	+
1445/1446	Y27T;L253V;F254W;A255G;N348R;K369C;T384P	+	+
1447/1448	Y27T;D74N;F254W;A255G;N348R;W370I;D381K	+	+
1453/1454	Y27T;D74N;L253V;F254W;N348R;W370I;D381F	+	+
1455/1456	Y27T;D74S;F254W;A255G;N348R;W370I;D381F;T384P	+	+
1457/1458	Y27T;D74G;L253V;F254W;A255G;D381K	+	+
1467/1468	Y27T;D74G;F254W;A255G;N348R;W370I	+	+
1469/1470	Y27T;D74G;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1479/1480	Y27T;D74S;L253V;N348R;D381W	+	+
1485/1486	Y27T;D74S;A255G	+	
1489/1490	Y27T;D74S;L253V;A255G;N348R;W370I;D381K	+	+
1493/1494	Y27T;D74N;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1495/1496	Y27T;D74S;F254W;A255G;W370I	+	+
1503/1504	Y27T;D74N;F254W;N348R	+	
1505/1506	Y27T;F254W;A255G;W370I	+	
1511/1512	Y27T;F254W;A255G;N348R;W370I	+	
1521/1522	Y27T;D74G;L253V;D381F;T384P	+	+
1533/1534	Y27T;D74P;W370I	+	
1543/1544	Y27T;D74N;L253V;F254W;A255G;W370I	+	+
1545/1546	Y27T;D74G;L253V;N348R;W370I	+	+
1567/1568	Y27T;L253V;F254W;N348R;W370I;T384P	+	+
1573/1574	Y27T;L253V;F254W;N348R;D381W;T384P	+	+
1577/1578	Y27T;L253V;F254W;A255G;G260C;N348R;D381F;T384P	+	+
1579/1580	Y27T;D74P;L253V;F254W;N348R;D381F;T384P	+	+
1581/1582	Y27T;D74G;L253V;F254W	+	+

[0291]

표 12.6 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	B1/B29 아실화 전환율(%) (FIOPC)[1]	B1/B29 아실화 선택성(%) (FIOPC)[2]
1585/1586	Y27T;D74N;L253V;N348R	+	+
1587/1588	Y27T;D74G;L253V;A255G;N348R;T384P	+	+
1589/1590	Y27T;D74N;L253V;A255G;W370I	+	+
1591/1592	Y27T;D74N;A255G;N348R;W370I	+	+
1597/1598	Y27T;D74P;F254W;A255G;N348R;D381K;T384P	+	+
1599/1600	Y27T;F254W;A255G;N348R;W370I;D381W;T384P	+	+
1601/1602	Y27T;L253V;A255G;N348R;K369C;W370I	+	
1605/1606	Y27T;D74S;A255G;N348R;D381K;T384P	+	+
1607/1608	Y27T;D74P;L253V;F254W;N348R;W370I;D381W;T384P	+	+
1609/1610	Y27T;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1613/1614	Y27T;D74G;F254W;N348R;D381W;T384P	+	+
1617/1618	Y27T;D74N;F254W;N348R;W370I	+	+
1619/1620	Y27T;D74P;L253V;F254W;N348R;K369C	+	+
1625/1626	Y27T;D74P;L253V;F254W;N348R	+	
1629/1630	Y27T;F254W;K369C;D381F;T384P	+	+
1631/1632	Y27T;L253V;F254W;N348R;W370I;D381F	+	+
1635/1636	Y27T;D74N;L253V;F254W;N348R;W370I	+	+
1641/1642	Y27T;F254W;N348R;K369C;W370I;D381N;T384P	+	+
1657/1658	Y27T;D74G;L253V;F254W;A255G;N348R	+	
1767/1768	D623N	+	+
1769/1770	T384R	+	+
1771/1772	D623L	+	+
1835/1836	F620R	++	+++
1837/1838	D709N	+++	+++
1859/1860	K128W	++	++
1861/1862	T705E	++	++
1869/1870	A255E	++	++
1873/1874	F254T	++	++

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 10배 미만의 활성 증가; "++" = 10배 초과 50배 미만의 활성 증가;
"+++" = 50배 초과 100배 미만의 활성 증가; "++++" = 100배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다:
"+" = 2배 초과 10배 미만의 선택성 증가; "++" = 10배 초과 50배 미만의 선택성 증가;
"+++" = 50배 초과 100배 미만의 선택성 증가; "++++" = 100배 초과의 선택성 증가.

[0292]

표 12.7 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B1/B29 아실화 선택성(%) (FIOPC)[2]
1313/1314	Y27T;L253V;A255G;N348R;T384P	+	+
1315/1316	Y27T;L253V	+	+
1317/1318	Y27T;D74G;L253V;F254W	+	+
1319/1320	Y27T;D74S;F254W;N348R;D381W	+	+
1321/1322	Y27T;D74G;A255G;N348R;K369C;D381F;T384P	+	+
1323/1324	Y27T;D74G;L253V;A255G;N348R;W370I;T384P	+	+
1325/1326	Y27T;D74N;L253V;F254W;N348R;W370I;D381K;T384P	++	+
1327/1328	Y27T;D74N;L253V;F254W;A255G;N348R;W370I	+	+
1329/1330	Y27T;A255G;N348R;W370I	++	+
1333/1334	Y27T;N348R;T384P	+	+
1335/1336	Y27T;D74G;L253V;N348R;K369C;W370I;D381F;T384P	+	+
1339/1340	Y27T;D74P;L253V;F254W;A255G;N348R	+	+
1341/1342	Y27T	+	+
1345/1346	Y27T;D74G;L253V;F254W;A255G;W370I	+	+
1347/1348	Y27T;L253V;F254W;A255G	+	+
1349/1350	Y27T;D74G;L253V;F254W;T384P	+	+
1351/1352	Y27T;D74N;F254W;N348R;W370I	+	+
1353/1354	Y27T;D74S;L253V;N348R;W370I;D381K;T384P	++	++
1355/1356	Y27T;L253V;N348R	+	+
1357/1358	Y27T;L253V;A255G;W370I	+	+
1359/1360	Y27T;D74G;F254W;A255G;D381F	+	+
1361/1362	Y27T;F254W;N348R;T384P	+	
1363/1364	Y27T;D74G;F254W;A255G;N348R;D381W	+	+

[0293]

[0294]

표 12.7 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B1/B29 아실화 선택성(%) (FIOPC)[2]
1367/1368	D74N;F254W;A255G;N348R;T384P	+	+
1369/1370	Y27T;F254W;A255G	+	+
1373/1374	Y27T;D74S;N348R	+	+
1375/1376	Y27T;D74P;F254W;A255G;N348R	+	+
1377/1378	Y27T;L253V;F254W;N348R;D381F	+	+
1381/1382	Y27T;D74S;L253V;A255G;T384P	+	+
1383/1384	Y27T;D74G;A255G;W370I	++	+
1387/1388	Y27T;D74N;L253V;N348R;W370I;D381W;T384P	++	++
1389/1390	Y27T;D74G;L253V;F254W;N348R	++	+
1393/1394	Y27T;D74P;L253V;N348R	+	+
1395/1396	Y27T;L253V;F254W;A255G;N348R	+	+
1397/1398	Y27T;D74S;L253V;F254W;A255G;N348R	+	+
1399/1400	Y27T;D74G;F254W;A255G;N348R;K369C;W370I;D381F	+	+
1401/1402	Y27T;D74P;F254W;A255G;N348R;K369C;W370I	+	+
1403/1404	Y27T;D74N;L253V;F254W;W370I;D381K	++	++
1405/1406	Y27T;D74G;F254W;K369C;W370I	+	+
1407/1408	Y27T;D74G;L253V;N348R;W370I	++	+
1409/1410	Y27T;D74G;L253V;T384P	+	+
1411/1412	Y27T;D74S;N348R;W370I	++	+
1415/1416	Y27T;D74G;A255G;N348R	+	+
1421/1422	Y27T;D74G;F254W;A255G;N348R	+	+
1423/1424	Y27T;L253V;N348R;W370I;T384P	++	+
1425/1426	Y27T;D74N;L253V;F254W;A255G	+	+
1433/1434	Y27T;F254W;A449V	+	+
1437/1438	Y27T;D74G;L253V;A255G;N348R;D381W	+	+
1439/1440	Y27T;D74P;L253V;W370I	+	+
1443/1444	Y27T;D74G;L253V;F254W;A255G;W370I;D381K;T384P	++	++
1447/1448	Y27T;D74N;F254W;A255G;N348R;W370I;D381K	+	+
1453/1454	Y27T;D74N;L253V;F254W;N348R;W370I;D381F	++	++
1455/1456	Y27T;D74S;F254W;A255G;N348R;W370I;D381F;T384P	++	++
1457/1458	Y27T;D74G;L253V;F254W;A255G;D381K	++	+
1459/1460	Y27T;D74S;F254W;K369L;W370I	+	+
1461/1462	Y27T;D74N;F254W;A255G;N348R;K369C;D381F	+	+
1463/1464	Y27T;L253V;F254W;D381F;T384P	++	+
1467/1468	Y27T;D74G;F254W;A255G;N348R;	++	++

표 12.7 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B1/B29 아실화 선택성(%) (FIOPC)[2]
	W370I		
1469/1470	Y27T;D74G;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1471/1472	L253V;N348R;W370I	+	+
1473/1474	Y27T;F254W;N348R;W370I	+	+
1479/1480	Y27T;D74S;L253V;N348R;D381W	++	++
1481/1482	Y27T;D74S;L253V;N348R	+	+
1485/1486	Y27T;D74S;A255G	+	+
1487/1488	Y27T;L253V;A255G;N348R	+	+
1489/1490	Y27T;D74S;L253V;A255G;N348R;W370I;D381K	+	+
1493/1494	Y27T;D74N;L253V;F254W;A255G;N348R;W370I;T384P	+	+
1495/1496	Y27T;D74S;F254W;A255G;W370I	++	+
1497/1498	Y27T;F254W;A255G;K369C;W370I;D381F;T384P	+	+
1499/1500	Y27T;A255G;N348R	+	+
1501/1502	Y27T;L253V;F254W;D381F	+	+
1503/1504	Y27T;D74N;F254W;N348R	+	+
1505/1506	Y27T;F254W;A255G;W370I	++	++
1507/1508	Y27T;L253V;N348R;D381F;T384P	+	+
1511/1512	Y27T;F254W;A255G;N348R;W370I	++	++
1513/1514	Y27T;L253V;F254W;N348R	+	+
1515/1516	Y27T;D74N;F254W	+	+
1519/1520	Y27T;D74N;F254W;N348R;K369C;D381F;T384P	+	+
1521/1522	Y27T;D74G;L253V;D381F;T384P	++	++
1523/1524	Y27T;D74P;L253V;A255G	+	+
1529/1530	Y27T;D74S;F254W;A255G;N348R;K369C;W370I	+	+
1533/1534	Y27T;D74P;W370I	++	+
1537/1538	Y27T;L253V;F254W;T384P	+	+
1539/1540	Y27T;D74N;N348R	+	+
1541/1542	Y27T;L253V;F254W;N348R;T384P	+	+
1543/1544	Y27T;D74N;L253V;F254W;A255G;W370I	+	+
1547/1548	Y27T;F254W;A255G;N348R	+	+
1549/1550	Y27T;D74S;F254W;N348R	+	+
1551/1552	Y27T;D74P;F254W;A255G;N348R;D381K;T384P	+	+
1553/1554	Y27T;F254W;A255G;N348R;W370I;T384P	++	++
1559/1560	Y27T;D74N;N348R;T384P	+	+
1561/1562	Y27T;D74S;K369C;W370I;D381K;T384P	+	+
1563/1564	Y27T;L253V;A255G;W370I;D381F;T384P	++	++

[0295]

표 12.7 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B1/B29 아실화 선택성(%) (FIOPC)[2]
1567/1568	Y27T;L253V;F254W;N348R;W370I;T384P	++	+
1569/1570	Y27T;D74N;F254W;N348R;W370I;D381K	+	+
1573/1574	Y27T;L253V;F254W;N348R;D381W;T384P	++	+
1575/1576	Y27T;L253V;F254W	+	+
1577/1578	Y27T;L253V;F254W;A255G;G260C;N348R;D381F;T384P	+	+
1579/1580	Y27T;D74P;L253V;F254W;N348R;D381F;T384P	++	++
1585/1586	Y27T;D74N;L253V;N348R	+	+
1587/1588	Y27T;D74G;L253V;A255G;N348R;T384P	+	+
1589/1590	Y27T;D74N;L253V;A255G;W370I	+	+
1591/1592	Y27T;D74N;A255G;N348R;W370I	+	+
1595/1596	Y27T;N348R	+	+
1599/1600	Y27T;F254W;A255G;N348R;W370I;D381W;T384P	++	++
1603/1604	Y27T;L253V;D381F;T384P	+	+
1605/1606	Y27T;D74S;A255G;N348R;D381K;T384P	+	+
1607/1608	Y27T;D74P;L253V;F254W;N348R;W370I;D381W;T384P	++	++
1609/1610	Y27T;L253V;F254W;A255G;N348R;W370I;T384P	++	+
1611/1612	A255G;N348R;W370I	+	+
1613/1614	Y27T;D74G;F254W;N348R;D381W;T384P	++	++
1615/1616	Y27T;F254W;A255G;D381K;T384P	++	++
1621/1622	Y27T;D74S;F254W;N348R;D381F	+	+
1625/1626	Y27T;D74P;L253V;F254W;N348R	+	+
1631/1632	Y27T;L253V;F254W;N348R;W370I;D381F	+	+
1633/1634	Y27T;D74G;L253V;A255G	+	+
1635/1636	Y27T;D74N;L253V;F254W;N348R;W370I	+	+
1643/1644	Y27T;D74G;L253V;F254W;A255G;N348R;K369C;W370I;D381F	+	+
1645/1646	Y27T;D74G;L253V;F254W;N348R;K369C;W370I	+	+
1647/1648	Y27T;A255G;N348R;D381W;T384P	+	+
1649/1650	Y27T;L253V;F254W;A255G;N348R;W370I	++	+
1651/1652	Y27T;F254W;N348R;D381W;T384P	+	+
1653/1654	Y27T;D74G;N348R	+	+
1655/1656	Y27T;D74N;L253V	+	+

[0296]

표 12.7 아실화 결과

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1288 대비)	A1/B1/B29 아실화 전환율(%) (FIOPC)[1]	A1/B1/B29 아실화 선택성(%) (FIOPC)[2]
1657/1658	Y27T;D74G;L253V;F254W;A255G;N348R	+	+
1717/1718	D623W	+	+
1743/1744	D623V	+	+
1747/1748	D623A	+	+
1749/1750	D381Q	+	+
1771/1772	D623L	+	+
1795/1796	D623N	+	+
1797/1798	T384R	++	+
1823/1824	A373K	+	+
1827/1828	F620R	+	+
1863/1864	F254T	+	+
1865/1866	A255P	+	+

[1] 전환율(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 2배 초과 10배 미만의 활성 증가; "++" = 10배 초과 50배 미만의 활성 증가; "+++" = 50배 초과의 활성 증가; "+++" = 50배 초과의 활성 증가.

[2] 선택성(%)은 서열 번호: 1288의 참조 폴리펩티드 대비로 측정되었고, 이는 하기와 같이 정의되었다: "+" = 2배 초과 10배 미만의 선택성 증가; "++" = 10배 초과 50배 미만의 선택성 증가; "+++" = 50배 초과의 선택성 증가.

[0297]

[0298] **실시예 13**

[0299] **대체 아실 공여자를 이용한 인슐린의 아실화**

[0300] 메틸 페닐아세테이트에 대한 대체물로서 (메틸 2-(4-하이드록시페닐)아세테이트 또는 2-(4-하이드록시페닐)아세트아미드)를 사용하여 표 13에 열거된 5개의 변이체의 아실화를 평가하였다. 실시예 4에 기술된 바와 같이 진탕 플라스크 분말을 제조하였다. 각각 0.1 M CHES, pH 10, 5% 아세토니트릴, 15 g/L 인슐린, 26 g/L 아실 공여자 (메틸 2-(4-하이드록시페닐)아세테이트 또는 2-(4-하이드록시페닐)아세트아미드) 및 1 g/L 동결건조된 효소 분말을 함유하는 96 웰 깊은 웰 플레이트 주에서 반응을 수행하였다. HTP 플레이트를 가열 밀봉하고, 써모트론® 진탕기(3 mm 쓰로우(throw), 모델 #AJ185, Infors) 중 30℃에서 300 rpm으로 2시간 동안 인큐베이션시켰다. 반응물을 200 ㎕ 아세토니트릴로 켄칭하고, 벤치 탑 진탕기를 사용하여 5분 동안 혼합하였다. 이어서, 플레이트를 4,000 rpm으로 5분 동안 원심분리하고, 분석을 위해 HPLC에 적재하였다.

[0301] 각 변이체의 활성은 HPLC 분석에 의해 측정된 바와 같은, 모든 생성물의 피크 면적을 기질 및 다양한 인슐리 생성물의 면적의 총합으로 나눔으로써 정량화된 전환율(%)로서 계산된다.

표 13

표 13.1

서열 번호: (nt/aa)	아미노산 차이 (서열 번호: 1262 대비)	2-(4-하이드록시페닐) 아세트아미드[1]	메틸 2-(4-하이드록시페닐) 아세테이트[1]
1287/1288	F71G;G74D	+++	+++
1007/1008	F24A;Y31W;V56I;F701W	++	+
1019/1020	F24A;Y31W;F71C;F701W	++	+
1023/1024	F24A;V56T;F701W	+	++
1031/1032	F24A;Y31W;V56I;F701Y	+	++

[1] 전환율(%)은 하기와 같이 정의되었다: "+" = 1% 초과 10% 미만의 전환; "++" = 10.0% 초과 20% 미만의 전환; "+++" = 20% 초과의 전환.

[0302]

[0303] **실시예 14**

[0304] **인슐린 및 그의 아실화된 생성물의 분석적 검출**

[0305] 표 14.1, 14.2, 14.3, 14.4, 및 14.5의 분석 방법을 사용하여 실시예 5-12에 기술된 데이터를 수집하였다. 본원

에 제공된 방법들은 모두 본 발명을 사용하여 제조된 변이체를 분석하는 데 사용된다. 도 1에 제시된 결과는 본 방법에 대한 화합물의 용출 순서에 상응하다.

표 14

표 14.1 분석 방법	
장치	써모(Thermo) LXQ
칼럼	워터스 X브릿지(Waters Xbridge) C18 칼럼: 50 x 3.0 mm, 5 um, 페노메넥스(Phenomenex) C18 가드 포함 카트리지: 5 x 3.0 mm, 5 μm
이동상	구배(A: 물 중 0.2% 포름산; B: MeCN 중 0.2% 포름산) 시간(min) %A 0.0 78 1.0 78 4.0 68 5.0 5.0 6.0 78 7.0 78
유속	0.7 mL/min
전개 시간	7 min
칼럼 온도	45 °C
주입 부피	10 μL
MS 검출	LXQ; 0-0.5 min 사이에 MS로부터 유동 우회 하기 생성물에 대한 BP 추출된 이온: 인슐린 생성물 = 968.6, 1162.6, 1453.0, 1937.0 모노-인슐린 생성물 = 1189.5, 1486.5, 1981.5 디-인슐린 생성물 = 1216.0, 11519.8 트리-인슐린 생성물 = 1243.0, 1553.5
MS 조건	MS 극성: 양성; 이온화: ESI; 모드: 300-2000으로부터의 Q1 스캔; 전원 전압: 20; 차단 가스: 40; Aux 가스: 10; 캡 온도: 350; 이온분무 전압: 5000; 캡 V: 5; 튜브 렌즈: 55.

[0306]

[0307]

표 14.2 분석 방법	
장치	애질런트 HPLC 1200 시리즈
칼럼	아센티스 익스프레스(Ascentis Express) C18, 4.6 x 100 또는 150 mm, 2.7 uM
이동상	구배 I(A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0.0 95 0.1 70 8, 8.5 또는 9 50 8.1, 8.6 또는 9.1 5 8.2, 8.7, 또는 9.2 95 9, 9.2 또는 9.5 95 구배 II (A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0 70 7 또는 8 50 7.1 또는 8.1 70 9 또는 10 70
유속	1.0 mL/min
전개 시간	~10 min
생성물 용출 순서	인슐린; A1-아실화된 인슐린; B 29-아실화된 인슐린; B1-아실화된 인슐린; 디-A1,B29-아실화된 인슐린; 디-A1, B1-아실화된 인슐린; 디-B1, B29-아실화된 인슐린; 트리-A1, B1, B29-아실화된 인슐린
칼럼 온도	40 °C
주입 부피	5 μL
검출	UV 218nm 및 280nm 검출기: MWD(애질런트 1200 시리즈); 슬릿 = 4 nm; 피크 폭 > 0.1 min; 참조 = 360; BW = 8

[0308]

표 14.3 분석 방법	
장치	애질런트 HPLC 1290 시리즈
칼럼	워터스 코텍스(Waters Cortecs) UPLC C18 2.1 x 50 mm, 1.6 uM
이동상	샘플에 대한 구배 (A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0.0 72 2.5 50 2.51-2.7 10 2.71 72 3 72 세액에 대한 구배 (A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0.0 72 1.7 0 1.71-2 72
유속	0.9 mL/min
전개 시간	3 min
생성물 용출 순서	인슐린; A1-아실화된 인슐린; B 29-아실화된 인슐린; B1-아실화된 인슐린; 디-A1,B29-아실화된 인슐린; 디-A1, B1-아실화된 인슐린; 디-B1, B29-아실화된 인슐린; 트리-A1, B1, B29-아실화된 인슐린
칼럼 온도	40 °C
주입 부피	0.5 μL
검출	UV 218nm 및 280nm 검출기: MWD(애질런트 1290 시리즈); 슬릿 = 4 nm; 피크 폭 > 0.1 min; 참조 = 360; BW = 8

표 14.4 분석 방법	
장치	애질런트 HPLC 1200 시리즈
칼럼	아센티스 익스프레스 C18, 4.6 x 100 또는 150 mm, 2.7 uM
이동상	구배 I (A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0.0 95 0.1 70 5, 6 또는 8 50 5.5, 6.5, 또는 8.1 5 5.7 또는 6.7 5 5.8, 6.8, 또는 8.2 95 6, 7, 또는 9 95
유속	1.0 mL/min
전개 시간	~10 min
생성물 용출 순서	인슐린; A1-아실화된 인슐린; B 29-아실화된 인슐린; B1-아실화된 인슐린; 디-A1,B29-아실화된 인슐린; 디-A1, B1-아실화된 인슐린; 디-B1, B29-아실화된 인슐린; 트리-A1, B1, B29-아실화된 인슐린
칼럼 온도	40 °C
주입 부피	5 μL
검출	UV 218nm 및 280nm 검출기: MWD(애질런트 1200 시리즈); 슬릿 = 4 nm; 피크 폭 > 0.1 min; 참조 = 360; BW = 8

[0309]

표 14.5 분석 방법	
장치	애질런트 HPLC 1290 시리즈
칼럼	워터스 코텍스 UPLC C18 2.1 x 50 mm, 1.6 uM
이동상	샘플에 대한 구배 (A: 물 중 0.05% TFA; B: MeCN 중 0.05% TFA) 시간(min) %A 0.0 72 1.5 50 1.51-1.7 10 1.71 72 2 72
유속	0.9 mL/min
전개 시간	3 min
생성물 용출 순서	인슐린; A1-아실화된 인슐린; B 29-아실화된 인슐린; B1-아실화된 인슐린; 디-A1,B29-아실화된 인슐린; 디-A1, B1-아실화된 인슐린; 디-B1, B29-아실화된 인슐린; 트리-A1, B1, B29-아실화된 인슐린
칼럼 온도	40 °C
주입 부피	0.5 μL
검출	UV 218nm 및 280nm 검출기: MWD(애질런트 1290 시리즈); 슬릿 = 4 nm; 피크 폭 > 0.1 min; 참조 = 360; BW = 8

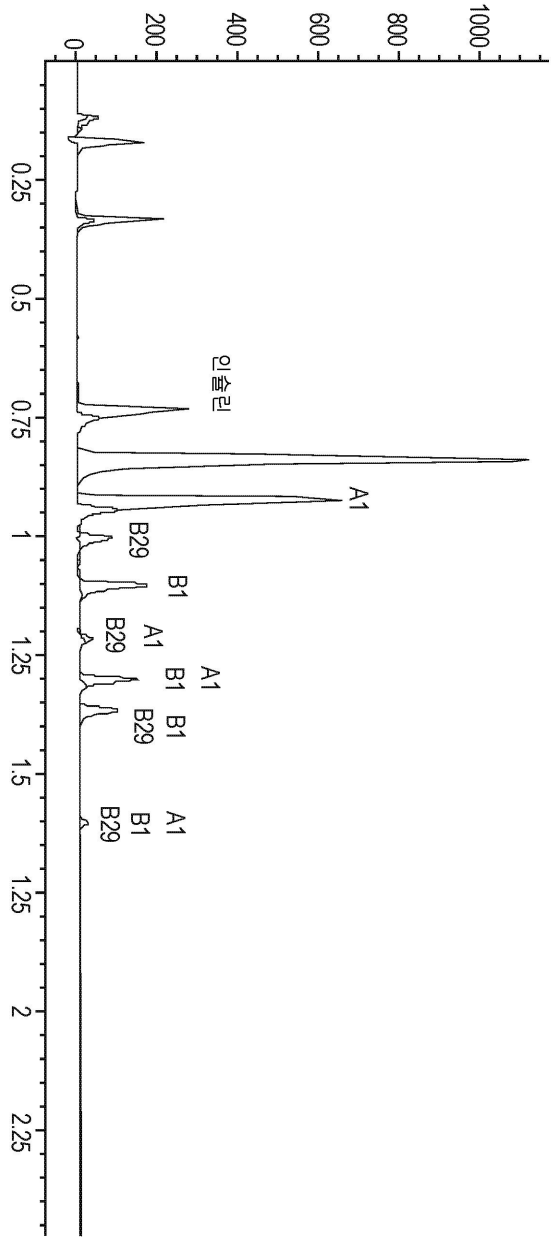
[0310]

[0311] 본 출원에서 인용된 모든 공개문헌, 특허, 특허 출원 및 다른 문헌들은 각각의 개별 공개문헌, 특허, 특허 출원 또는 다른 문헌이 모든 목적을 위해 참조로 포함되는 것으로 개별적으로 명시된 것과 같은 정도로 모든 목적을 위해 그 전문이 본원에서 참조로 포함된다.

[0312] 다양한 구체적인 실시양태가 예시되고 기술되었지만, 본 발명(들)의 정신 및 범주로부터 벗어남 없이, 다양하게 변형될 수 있다는 것을 이해할 것이다.

도면

도면1


0
200
400
600
800
1000
0.25
0.5
0.75
1
1.25
1.5
1.25
2
2.25
인슐린
A1
B29
B1
A1
B29
A1
B1
B1
B29
A1
B1
B29

도면2a

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1263/1264	V28A;G74D;Q547K;	+	+++++			+							
953/954	W431R;	+	+++++			+							
955/956	F701L;	+	+++++										
957/958	F701A;	+	+++++										
1265/1266	F701Y;	+	+++++			+							
959/960	F24A;	+	+++++			+							+
1267/1268	F71L;	+	+++++			+		+					
961/962	F71V;	+	+++++				+						
1269/1270	F71C;	+	+++++			+							
963/964	F71K;	+	+++			+		+					
1271/1272	F71R;		+++++										
965/966	F71E;	+	+++++			+							
967/968	F24Y;V28A;	+	+++++			+		+					
969/970	M697L;	+	+++++			+							

도면2b

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1273/1274	V56T;	+	+++++										
1275/1276	V56I;	+	+++++										
1277/1278	V56L;	+	+++++										
971/972	I177T;	+	+++++										
1281/1282	W154F;	+	+++++										
973/974	W154F;L754P;	+	+++++										
975/976	F71C;G74D;	+	+++	+	+			+					
1285/1286	F71Q;G74D;P164S;	+	+++	+	+				+				
1287/1288	F71G;G74D;	++	+++	+	+	+	+			+			
979/980	F701H;	+	+++++										
981/982	F701C;	+	+++++		+								
983/984	F701I;	++	+++++										
985/986	F701M;	+	+++++		+				+				
1289/1290	F701W;	+	+++++		+								

도면2c

서열 번호 : (nt/aa)	(서열 번호 : 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1291/1292	F701V;	+	++++										
987/988	M697F;	+	++++					+	+				
989/990	M697G;	+	++++					+	+				+
991/992	V28A;Y31F;		+++		‡								
993/994	V28A;Y31L;	+	++++		+								
995/996	V28A;Y31V;	+	+++		‡								
997/998	V28A;Y31T;	+	++++		+								
999/1000	V28A;Y31C;	+	++++		+								
1001/1002	V28A;Y31N;		+++		+++								
1003/1004	V28A;Y31M;	+	++++										
1005/1006	V28A;Y31K;		+++		‡								
1007/1008	F24A;Y31W;V56I;F701W;	+	++++										
1009/1010	F24A;V56I;F701W;	+	++++					+					
1011/1012	F24A;Y31C;V56I;S386P;F701												

도면2d

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
	Y;												
1013/1014	F24A;F71C;F701W;	+	++++										
1293/1294	F24A;P29S;V56L;T352S;N483S;		+++	+	‡								
1261/1262		+	++++	+									
1015/1016	F24A;L225V;F701Y;	+	++++										+
1017/1018	F24A;Y31W;V56T;V264A;F701W;S750G;		+++		‡								
1019/1020	F24A;Y31W;F71C;F701W;	+	++++		+								
1295/1296	F24A;Q340R;V391G;		+++		‡								
1021/1022	F24A;D484N;F701W;	‡	++++										
1023/1024	F24A;V56T;F7	‡	++++										

도면2e

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
	01W;												
1025/1026	F24A;Y31W;	+	++++										
1027/1028	F24A;V56I;W154F;I270V;M697L;		+++		‡								
1297/1298	F24A;Y31H;V56I;F71C;		+++		‡								
1029/1030	F24A;V56I;M697F;F701W;	+	++++		+								
1299/1300	F24A;V56L;W240R;F701W;		++++										
1031/1032	F24A;Y31W;V56I;F701Y;	+	++++		+								+
1301/1302	F24A;V56T;F71C;		+++		‡								
1303/1304	F24A;F71L;	+	++++		+								
1033/1034	F24A;Y31W;V56I;M697L;	+	++++		+								

도면2f

서열 번호: (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1035/1036	F24Y;V28A;F71C;F701W;	+	+++++			+	+	+					
1037/1038	F24Y;V28A;V56I;A308T;T379A;F701W;	+	+++++			+	+		+				
1039/1040	F24Y;V28A;D321N;F701H;	+	+++++										
1041/1042	F24Y;V28A;N457Y;F701W;	++	+++++										
1043/1044	F24Y;V28A;V56I;F701W;	+	+++++										
1045/1046	F24Y;Y27C;V28T;F701W;V729F;	+	+++++		+								
1305/1306	V56L;I77T;F701W;	+	+++++										
1047/1048	V56T;F71G;F701W;	++	+++++										
1049/1050	M697L;F701Y;	+	+++++		+								

도면2g

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1307/1308	W26C;F701W;		++++		+								
1051/1052	V56T;W658R;F701W;	+	++++		+								
1053/1054	V56T;F71G;F701I;	+	++++		+								
1055/1056	A410P;M697F;F701W;	+	++++		+								+
1057/1058	V56L;K322R;M697L;F701V;	+	++++										
1059/1060	V56L;F701H;	+	++++		+								
1061/1062	Y31C;V56L;F701H;	+	++++						+				
1063/1064	F71G;F701W;	‡	++++										
1065/1066	T129A;I511F;F701Y;		++++		+								
1309/1310	D501N;F701W;	+	++++		+								
1067/1068	V56T;F701W;L711Q;	+	++++		+								

도면2h

서열 번호 : (nt/aa)	(서열 번호: 1262 대비) 아미노산 차이	A1		B29		B1		A1/B29		A1/B1		B1/B29	
		전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]	전환율(%)[1]	선택성(%)[2]
1069/1070	I423T;F701W;	+	+++++			+							
1071/1072	V56I;W154F;F701W;	+	+++++			+							
1073/1074	V56L;W119R;K146E;F701Y;		+++			+							
1075/1076	V56T;M697L;F701W;	+	++++										
1311/1312	V56T;F701W;	+	+++++			+							

1 전환율(%)은 하기와 같이 정의되었다: "+" = 1% 초과 10% 미만의 전환율; "++" = 10.0% 초과 20% 미만의 전환율;"+++" = 20% 초과의 전환율.

2 선택성(%)은 하기와 같이 정의되었다: "+" = 5% 초과 20% 미만의 선택성; "++" = 20% 초과 40% 미만의 선택성;"+++" = 40% 초과 60% 미만의 선택성;"++++" = 60% 초과 80% 미만의 선택성;"+++++" = 80% 초과

서 열 목 록

SEQUENCE LISTING

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<120> PENICILLIN-G ACYLASES

<130> CX2-154WO1

<140> To Be Assigned

<141> 2017-05-05

<150> US 62/332,103

<151> 2016-05-05

<160> 1902

<170> PatentIn version 3.5

<210> 1

<211> 2541

<212> DNA

<213> Artificial Sequence

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tccgaggtgc tgggcaaagc attcgtcagt tttgataaag atattcgcca gaactactgg 300

ccggattcta ttcgcgcgca gatagcttcc ctctccgctg aggataaatc cattctgcag 360

ggctatgccg atggcatgaa tgcgtggatc gataaagtga acgccagccc cgataagctg 420

ttaccccagc agttctccac ctttggtttt aaacccaagc attgggaacc gtttgatgtg 480

gcgatgattt ttgtcggcac catggcgaac cggttttctg acagcaccag cgaaattgat 540

aacctggcgc tgctgacggc gctaaaagat aaatacggca agcagcaggg catggcggtc 600

tttaaccagc tgaaatggct ggttaatcct tccgcgccaa ccaccattgc ggcgcgggaa 660

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tacgaccagc cggcaccgat gctcgaccgc ccggcaaaag ggaccgatgg cgcgctgctg 780

gcgctgaccg ccgatcagaa ccgggaaact atcgccgcgc agttcgcgca aagcggcgct 840

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caggatgcga aggccattat ggtcaatggg ccgcagtttg gttggtatgc gccggcgtac 960

acctacggta tcggcctgca cggcgcgggc tatgacgtca ccggcaatac gccgtttgcc 1020

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<211> 846
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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35 40 45
Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln Asp
50 55 60
Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr Val
65 70 75 80
Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile Arg
85 90 95
Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu Ser
100 105 110
Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn Ala
115 120 125
Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln Gln
130 135 140
Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp Val
145 150 155 160
Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser Thr
165 170 175
Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys Tyr
180 185 190
Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu Val
195 200 205
Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr Pro
210 215 220

Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala Ala Leu Leu Pro Arg

225 230 235 240

Tyr Asp Gln Pro Ala Pro Met Leu Asp Arg Pro Ala Lys Gly Thr Asp

245 250 255

Gly Ala Leu Leu Ala Leu Thr Ala Asp Gln Asn Arg Glu Thr Ile Ala

260 265 270

Ala Gln Phe Ala Gln Ser Gly Ala Asn Gly Leu Ala Gly Tyr Pro Thr

275 280 285

Thr Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys

290 295 300

Ala Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr

305 310 315 320

Thr Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn

325 330 335

Thr Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile

340 345 350

Ser Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala

355 360 365

Glu Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu

370 375 380

Trp Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly

385 390 395 400

Gln Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile

405 410 415

Lys Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp

420 425 430

Asp Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys

435 440 445

Ala Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu

450 455 460

Thr Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val

465 470 475 480

His Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu

485 490 495

Pro Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe

500 505 510

Asp Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn

515 520 525

Trp Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala

530 535 540

Phe Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu

545 550 555 560

Asp Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg

565 570 575

Gln Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu

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Lys Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu

595 600 605

Val Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp

610 615 620

Gly Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu

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Gly Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro

660 665 670

Thr Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala

675 680 685

Leu Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly

690 695 700

Gly Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp

705 710 715 720

Gln Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr
725 730 735
Pro Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro

740 745 750
Gln Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg
755 760 765
Gly Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg
770 775 780
Pro Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile
785 790 795 800
Ala Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met

805 810 815
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<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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<212> PRT

<213> Artificial Sequence

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<223> Penicillin-G Acylates Variant from K. citrophila

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

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305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

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370 375 380

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385 390 395 400

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405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

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<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gccggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 6

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 6

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Asn Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Ala Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Lys Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 7
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 7
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 8

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 8

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 9

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt tgcggtgatg gggtcgatat ctttgccgaa 240

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gatgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 10

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 10

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 11

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 11

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgtgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gatgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt tcggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccct ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 12

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 12

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Phe Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 13

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 13

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 14

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 14

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 15

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 15

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca ataccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 16

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 16

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 17

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 17

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgaa aaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 18

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 18

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Lys Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 19

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 19

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 20

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 20

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 21

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 21

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaacaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 22

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 22

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 23
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 23
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 24

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 24

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 25

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 25

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagcaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 26
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 26
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 27

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 27

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 28

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 28

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 29

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 29

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggcggtct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 30

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 30

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Gly Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 31
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 31

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 32

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 32

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 33
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 33
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca caggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 34

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 34

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 35
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 35
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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgcg taacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 36

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 36

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Arg Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 37

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 37

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatattt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 38

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 38

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 39
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 39
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattatt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 40

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 40

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 41

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 41

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac agtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 42

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 42

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 43

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 43

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 44

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 44

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 45

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 45

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggcgcact gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 46

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 46

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ala Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 47

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 47

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcatg gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 48

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 48

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Trp Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 49

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 49

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccaccga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 50

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 50

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Thr Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 51
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 51
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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 52

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 52

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 53

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 53

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 54

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 54

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 55

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 55

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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg taccttgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 56

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 56

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 57

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 57

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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 58

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 58

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 59

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 59

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcatt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 60

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 60

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 61

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 61

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccgc aaacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 62

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 62

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Ala Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 63
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 63

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagagtgt cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 64

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 64

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 65

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 65

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 66

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 66

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 67
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 67
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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacctat 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccct taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 68

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 68

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Tyr Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Leu Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 69

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 69

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggccatct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 70

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 70

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly His Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 71
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 71
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcaaaa gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 72

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 72

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Lys Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 73

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 73

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 74

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 74

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 75

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 75

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 76

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 76

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 77

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 77

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 78

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 78

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 79
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 79

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgagtct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 80
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 80

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Ser
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 81

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 81

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 82

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 82

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Cys Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 83

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 83

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ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccatg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 84

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 84

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 85

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 85

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 86

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 86

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 87

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 87

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 88

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 88

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Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
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225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 89

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 89

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 90

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 90

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 91

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 91

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 92

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 92

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 93
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 93

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 94

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 94

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 95

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 95

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 96

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 96

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 97
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 97
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 98

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 98

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 99
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 99
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 100

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 100

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 101

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 101

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 102

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 102

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 103
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 103
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 104

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 104

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 105

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 105

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 106
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 106
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 107

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 107

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 108

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 108

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 109

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 109

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840

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ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 110

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 110

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 111

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 111

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 112

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 112

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

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645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 113

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 113

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 114

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 114

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 115

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 115

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 116

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 116

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 117

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 117

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 118

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 118

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 119

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 119

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 120

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 120

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 121

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 121

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 122

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 122

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 123

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 123

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 124

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 124

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 125
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 125

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 126

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 126

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 127
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 127

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 128

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 128

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 129

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 129

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 130

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 130

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 131
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 131
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 132

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 132

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 133

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 133

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
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acgcaaacgg cgtaa 2295

<210> 134

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 134

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 135

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 135

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 136
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 136

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 137

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 137

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 138

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 138

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 139

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 139

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 140

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 140

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 141
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 141

agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 142

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 142

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 143
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 143

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 144

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 144

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 145
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 145
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 146

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 146

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 147
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 147
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 148

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 148

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 149

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 149

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 150

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 150

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 151
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 151
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 152

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 152

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 153

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 153

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 154

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 154

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 155

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 155

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 156

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 156

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 157

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 157

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 158

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 158

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 159

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 159

agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 160

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 160

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 161

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 161

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 162

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 162

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 163
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 163
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 164

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 164

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 165

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 165

agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggatatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 166

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 166

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 167

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 167

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 168

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 168

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 169

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 169

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 170

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 170

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 171

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 171

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 172

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 172

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 173

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 173

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 174

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 174

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 175
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 175

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 176

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 176

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 177

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 177

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 178

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 178

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 179
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 179
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agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 180

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 180

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 181

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 181

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 182

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 182

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 183

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 183

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 184

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 184

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 185

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 185

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 186

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 186

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 187

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 187

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 188

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 188

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 189

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 189

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 190

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 190

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 191
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 191

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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acgcaaacgg cgtaa 2295

<210> 192
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 192
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 193

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 193

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 194

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 194

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 195

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 195

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 196

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 196

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 197

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 197

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840

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ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 198

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 198

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 199

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 199

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 200

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 200

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 201

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 201

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 202

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 202

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp

260 265 270

Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 203

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 203

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 204

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 204

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 205
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 205

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 206

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 206

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 207

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 207

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 208

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 208

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 209
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 209
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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 210

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 210

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 211
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 211
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 212

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 212

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 213

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 213

agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 214

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 214

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 215
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 215
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 216

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 216

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 217

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 217

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcacagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 218
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 218
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 219

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 219

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 220

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 220

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 221

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 221

agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 222

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 222

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 223

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 223

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960

gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 224

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 224

Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 225

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 225

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 226

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 226

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 227

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 227

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccag taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 228

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 228

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Ser Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 229

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 229

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagcta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 230

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 230

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 231

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 231

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 232

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 232

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 233

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 233

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 234

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 234

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 235

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 235

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 236

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 236

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 237
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 237

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 238

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 238

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 239
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 239

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcccttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 240

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 240

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 241

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 241

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 242

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 242

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 243
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 243
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 244

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 244

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 245

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 245

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 246

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 246

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 247

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 247

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 248
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 248

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 249

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 249

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 250

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 250

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 251

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 251

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 252

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 252

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 253
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 253

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 254

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 254

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 255
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 255

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 256

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 256

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu Tyr Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 257
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 257
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaacaga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 258

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 258

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 259
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 259
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 260

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 260

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 261

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 261

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 262

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 262

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 263
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 263
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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 264

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 264

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 265

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 265

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 266

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 266

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 267

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 267

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 268

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 268

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 269

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 269

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 270

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 270

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 271

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 271

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 272

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 272

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 273

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 273

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 274

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 274

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 275

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 275

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 276

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 276

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 277

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 277

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 278

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 278

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 279

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 279

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcttgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagcta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 280

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 280

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 281

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 281

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 282

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 282

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 283

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 283

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 284

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 284

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 285

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 285

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaaaaca ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 286

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 286

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 287
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 287

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 288

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 288

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 289

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 289

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 290

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 290

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 291

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 291

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 292

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 292

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 293

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 293

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 294

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 294

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 295

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 295

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 296

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 296

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 297

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 297

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 298

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 298

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 299

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 299

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 300

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 300

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 301

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 301

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 302

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 302

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 303
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 303

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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acgcaaacgg cgtaa 2295

<210> 304
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 304
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 305

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 305

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 306

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 306

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 307

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 307

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 308

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 308

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 309

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 309

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 310

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 310

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 311

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 311

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaacaga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 312

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 312

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 313

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 313

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaggtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 314

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 314

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 315

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 316

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 316

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 317
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 317

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgagtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 318

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 318

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Glu Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 319

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 319

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 320

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 320

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 321
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 321
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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acgcaaacgg cgtaa 2295

<210> 322

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 322

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

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610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 323
<211> 2295
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<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 323
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 324

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 324

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 325

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 325

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 326

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 326

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 327

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 327

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 328

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 328

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 329

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 329

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 330
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 330
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 331

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 331

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 332

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 332

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 333

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 333

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 334

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 334

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 335

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 335

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 336

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 336

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 337

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 337

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 338

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 338

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 339

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 339

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 340

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 340

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 341

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 341

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 342

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 342

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 343

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 343

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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acgcaaacgg cgtaa 2295

<210> 344

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 344

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 345

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 345

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 346

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 346

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 347

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 347

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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acgcaaacgg cgtaa 2295

<210> 348

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 348

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
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610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 349

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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acgcaaacgg cgtaa 2295

<210> 350

<211> 764

<212> PRT

<213> Artificial Sequence

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><223> Penicillin-G Acylates Variant from K. citrophila

<400> 350

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
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260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

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Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

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545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

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<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 351

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 352

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 352

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 353

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 353

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 354

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 354

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 355
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 355
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 356

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 356

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 357

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 357

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 358

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 358

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 359

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 359

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 360
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 360

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 361

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 361

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 362

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 362

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 363

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 363

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 364

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 364

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 365
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 365

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

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acgcaaacgg cgtaa 2295

<210> 366

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 366

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 367
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 367

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggatatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

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acgcaaacgg cgtaa 2295

<210> 368

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 368

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 369
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 369
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 370

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 370

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ser Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 371
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 371
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 372

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 372

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 373

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 373

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 374

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 374

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 375
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 375
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 376

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 376

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 377

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 377

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 378

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 378

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 379

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 379

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 380

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 380

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 381

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 381

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcccttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 382

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 382

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 383

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 383

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 384

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 384

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 385

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 385

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 386

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 386

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 387

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 387

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 388

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 388

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 389

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 389

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 390

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 390

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 391

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 391

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 392

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 392

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 393

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 393

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 394

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 394

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 395

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 395

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 396

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 396

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 397

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 397

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaaaaca ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 398

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 398

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 399
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 399

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 400

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 400

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 401

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 401

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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acgcaaacgg cgtaa 2295

<210> 402

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 402

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 403
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 403
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 404

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 404

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 405

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 405

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 406

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 406

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 407

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 407

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcccttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 408

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 408

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 409

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 409

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 410

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 410

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 411

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 411

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aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 412

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 412

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 413

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 413

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acgcaaacgg cgtaa 2295

<210> 414

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 414

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Gln Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 415
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 415

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 416
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 416

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40				45					

Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55				60					
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70				75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85				90					95			
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 417

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 417

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 418

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 418

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 419

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 419

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggatggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 420

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 420

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 421

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 421

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 422

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 422

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 423

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 423

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 424

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 424

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 425

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 425

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 426

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 426

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 427

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 427

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgggttgta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 428

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 428

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Gly Cys Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 429
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 429

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagtgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 430

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 430

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 431

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 431

agcaatatgt gggtgattgg caaagataaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 432

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 432

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 433

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 433

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggt 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 434

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 434

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 435
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 435
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 436

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 436

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 437

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 437

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccc aatggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 438

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 438

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 439
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 440

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 440

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 441

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 441

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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acgcaaacgg cgtaa 2295

<210> 442
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 442
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 443

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 443

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 444

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 444

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 445

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 445

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 446

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 446

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 447

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 447

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 448

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 448

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 449

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 449

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc taaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 450

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 450

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn

690 695 700

Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 451

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 451

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 452

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 452

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 453

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 453

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 454

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 454

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 455

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 455

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca acaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 456

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 456

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 457

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 457

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 458

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 458

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
690 695 700

Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 459

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 459

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccatg 1140

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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acgcaaacgg cgtaa 2295

<210> 460

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 460

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 461
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 461

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 462

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 462

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 463
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 463

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 464

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 464

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 465
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<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 465
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

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ttctctgaca acaccaccga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 466

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 466

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
690 695 700

Thr Thr Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 467
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacttggcca gtggctatga aaccacccag 1140

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 468

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 468

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 469

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 469

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acgcaaacgg cgtaa 2295

<210> 470

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 470

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Cys Arg His Gln Cys Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 471

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 471

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca acaccaccga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 472

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 472

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
690 695 700
Thr Thr Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 473

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 473

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccaccatg 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc taaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 474

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 474

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 475

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 475

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggcagtct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcatg gaaagagtgc cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 476

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 476

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Trp Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn

690 695 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 477
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 477

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacttggcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcact aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 478

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 478

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 479
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 479

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 480

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 480

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 481
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 481
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc taaagagtgc cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 482

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 482

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 483
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 483
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 484

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 484

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 485

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 485

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 486

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 486

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 487
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 487
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 488

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 488

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 489

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 489

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 490

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 490

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 491

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 491

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 492

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 492

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 493

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 493

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 494

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 494

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 495

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 495

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 496

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 496

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 497

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 497

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 498

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 498

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 499

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 499

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 500

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 500

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 501

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 501

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 502

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 502

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 503

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 503

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 504

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 504

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 505

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 505

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 506

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 506

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 507

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 507

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 508

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 508

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 509
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 509

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 510

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 510

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 511
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 511

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

gacaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 512

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 512

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Asp Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 513

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 513

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 514

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 514

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 515
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 515
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 516

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 516

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 517

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 517

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 518

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 518

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 519

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 519

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 520

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 520

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 521

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 521

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 522

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 522

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 523

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 523

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagacccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 524

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 524

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Arg Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 525

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 525

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 526

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 526

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 527
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 527

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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<210> 528
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 528

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
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Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55				60					
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70				75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85				90					95			
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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465                 470                 475                 480
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            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 529

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 529

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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acgcaaacgg cgtaa 2295

<210> 530

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 530

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
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500 505 510
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515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

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Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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<210> 531

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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acgcaaacgg cgtaa 2295

<210> 532

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<212> PRT

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><223> Penicillin-G Acylates Variant from K. citrophila

<400> 532

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
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580 585 590
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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

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645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

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<211> 2295

<212> DNA

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<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 533

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 534

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 534

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Asn Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 535

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 535

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 536

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 536

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 537

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 537

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 538

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 538

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 539

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 539

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 540

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 540

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 541
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 541

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 542

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 542

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 543

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 543

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 544

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 544

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 545
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 545
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 546

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 546

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 547
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 547
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 548

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 548

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 549

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 549

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 550

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 550

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 551
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 552

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 552

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 553

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 553

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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<210> 554
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

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Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 555

<211> 2295

<212> DNA

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<220><223> Penicillin-G Acylates Variant from K. citrophila

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 556

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 557

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 557

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 558

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 558

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 559

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 560

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 560

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 561

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 561

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 562

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 562

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 563

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 563

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 564

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 564

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 565

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 565

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 566

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 566

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 567

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 567

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 568

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 568

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 569

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 569

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 570

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 570

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 571

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 571

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 572

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 572

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 573
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 573

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 574

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 574

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 575
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 575

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 576

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 576

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 577

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 577

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 578

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 578

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 579
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 579
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 580

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 580

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 581

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 581

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 582

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 582

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 583

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 583

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 584

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 584

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 585

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 585

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 586

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 586

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 587

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 587

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 588

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 588

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 589
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 589

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 590

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 590

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 591
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 591

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 592

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 592

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 593
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 593
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 594

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 594

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 595
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 595
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 596

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 596

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 597

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 597

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc agtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 598

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 598

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 599

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 599

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 600

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 600

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 601

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 601

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acacaaacgg cgtaa 2295

<210> 602

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 602

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 603

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 603

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 604

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 604

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 605

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 605

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 606

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 606

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 607

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 607

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 608

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 608

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 609

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 609

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 610

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 610

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 611

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 611

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 612

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 612

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 613

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 613

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acgcaaacgg cgtaa 2295

<210> 614

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 614

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro

435 440 445

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Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 615

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 615

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

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<210> 616

<211> 764

<212> PRT

<213> Artificial Sequence

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><223> Penicillin-G Acylates Variant from K. citrophila

<400> 616

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35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 617

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 617

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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acgcaaacgg cgtaa 2295

<210> 618

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 618

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 619

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 619

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccccgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 620

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 620

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 621

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 621

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 622

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 622

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 623
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 623

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 624

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 624

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

```
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 625

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 625

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 626

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 626

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 627
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 628

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 628

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 629

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 630

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 630

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 631

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 631

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 632

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 632

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 633

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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acgcaaacgg cgtaa 2295

<210> 634

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 634

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 635

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 635

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 636

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 636

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 637

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 637

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 638

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 638

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 639
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 639

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 640
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 640

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40				45					

Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55				60					
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70				75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85				90					95			
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 641

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 641

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 642

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 642

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 643

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 643

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 644

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 644

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 645

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 645

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 646

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 646

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 647

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 647

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 648

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 648

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 649

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 649

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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acgcaaacgg cgtaa 2295

<210> 650

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 650

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 651

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 652

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 652

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 653
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 653

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 654

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 654

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 655

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 655

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 656

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 656

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 657
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 657
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 658

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 658

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Met Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 659
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 659
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 660

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 660

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 661

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 661

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 662

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 662

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 663

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 663

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 664

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 664

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 665

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 665

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 666
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 666
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 667

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 667

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 668

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 668

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 669

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 669

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 670

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 670

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 671

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 671

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 672

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 672

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 673

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 673

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 674

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 674

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 675

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 675

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 676

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 676

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Glu Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 677

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 677

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 678

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 678

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 679

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 679

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 680

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 680

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 681

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 681

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 682

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 682

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
```

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 683

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 683

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 684

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 684

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 685
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 685

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 686

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 686

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 687
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 687

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 688

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 688

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 689

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 689

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 690

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 690

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 691
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 691
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 692

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 692

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 693

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 693

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 694

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 694

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 695

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 695

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 696

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 696

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 697

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 697

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 698

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 698

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 699

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 699

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcca 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 700

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 700

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 701
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 701

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 702

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 702

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 703
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 703

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 704

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 704

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 705
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 705
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 706

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 706

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 707
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 707
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 708

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 708

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 709

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 709

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 710

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 710

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 711
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 711
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 712

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 712

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 713

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 713

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 714

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 714

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 715

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 715

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 716

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 716

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 717

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 717

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 718

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 718

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 719

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 719

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 720

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 720

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 721

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 721

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 722

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 722

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 723

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 723

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 724

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 724

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 725

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 725

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 726

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 726

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 727

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 727

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 728

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 728

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asn Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 729

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 729

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 730

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 730

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 731

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 731

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 732

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 732

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 733

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 733

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 734

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 734

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 735
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 735

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 736

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 736

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 737

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 737

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 738

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 738

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 739

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 739

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 740

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 740

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 741

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 741

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 742

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 742

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 743

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 743

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 744

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 744

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 745

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 745

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 746

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 746

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 747

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 747

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 748

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 748

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 749

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 749

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 750

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 750

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 751
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 751

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 752
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 752

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40				45					

Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55				60					
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70				75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85				90					95			
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 753

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 753

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 754

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 754

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 755

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 755

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 756

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 756

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 757

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 757

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 758

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 758

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 759

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 759

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 760

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 760

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 761

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 761

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 762

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 762

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 763

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 763

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 764

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 764

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 765
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 765

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 766

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 766

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 767

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 767

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 768

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 768

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 769
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 769
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 770

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 770

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 771
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 771
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 772

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 772

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 773

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 773

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 774

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 774

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 775
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 775
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 776

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 776

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 777

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 777

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 778
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 778
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 779

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 779

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 780

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 780

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 781

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 781

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 782

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 782

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 783

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 783

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 784

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 784

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 785

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 785

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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acgcaaacgg cgtaa 2295

<210> 786

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 786

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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755 760

<210> 787

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 787

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 788

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 788

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 789

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 789

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 790

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 790

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 791

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 791

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 792

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 792

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 793

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 793

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 794

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 794

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 795

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 795

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 796

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 796

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 797
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 797

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 798

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 798

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 799
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 799

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 800

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 800

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 801
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 801
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 802

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 802

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 803
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 803
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 804

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 804

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 805

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 805

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 806

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 806

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 807

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 807

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 808
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 808

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 809

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 809

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 810

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 810

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 811

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 811

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 812

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 812

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 813
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 813

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 814

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 814

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 815
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 815

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 816

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 816

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 817
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 817
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggca atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 818

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 818

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 819
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 819
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 820

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 820

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 821

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 821

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 822

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 822

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 823
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 823
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 824

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 824

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 825

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 825

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcggcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 826

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 826

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Arg Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 827

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 827

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 828

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 828

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 829

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 829

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 830

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 830

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 831

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 831

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 832

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 832

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 833

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 833

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 834

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 834

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 835

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 835

agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 836

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 836

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 837

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 837

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

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gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 838

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 838

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 839

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 839

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 840

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 840

Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 841

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 841

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 842

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 842

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 843

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 843

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 844

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 844

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 845

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 845

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 846

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 846

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 847
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 847

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 848

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 848

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 849

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 849

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 850

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 850

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 851
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 851
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 852

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 852

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 853

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 853

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 854

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 854

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 855

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 855

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcaaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 856

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 856

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 857

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 857

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 858

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 858

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 859

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 859

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 860

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 860

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 861

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 861

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 862

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 862

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 863
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 863

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 864
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 864

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 865

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 865

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 866

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 866

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 867

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 867

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaatggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 868

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 868

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 869

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 869

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 870

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 870

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 871

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 871

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 872

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 872

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 873

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 873

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 874

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 874

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 875

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 875

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 876

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 876

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 877
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 877

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 878

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 878

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 879

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 879

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 880

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 880

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 881
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 881
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 882

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 882

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 883
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 883
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 884

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 884

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 885

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 885

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

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acgcaaacgg cgtaa 2295

<210> 886

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 886

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 887

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 887

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 888

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 888

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 889

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 889

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgcgtct gtggggcggt 780

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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 890
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 890
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Arg
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 891

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 891

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 892

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 892

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 893

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 893

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 894

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 894

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 895

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 895

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 896

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 896

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 897

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 897

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 898

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 898

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 899

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 899

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 900

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 900

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 901

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 901

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 902

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 902

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 903

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 903

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 904

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 904

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 905

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 905

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 906

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 906

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 907

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 907

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 908

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 908

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 909
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 909

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 910

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 910

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 911
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 911

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 912

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 912

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 913

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 913

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 914

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 914

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 915
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 915
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 916

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 916

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 917

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 917

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 918

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 918

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 919

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 919

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 920

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 920

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 921

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 921

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 922

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 922

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 923

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 923

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 924

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 924

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 925
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 925

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 926

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 926

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 927
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 927

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 928

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 928

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 929
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 929
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 930

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 930

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 931
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 931
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 932

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 932

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 933

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 933

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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acgcaaacgg cgtaa 2295

<210> 934

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 934

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 935
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 936

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 937

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 937

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 938

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 938

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 939

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 939

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 940

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 940

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 941

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 941

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 942

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 942

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 943

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 943

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 944

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 944

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 945

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 945

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 946

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 946

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 947

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 947

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 948

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 948

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 949

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 949

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 950

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 950

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 951

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 951

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

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tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 952

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 952

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 953

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 953

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct cgccagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 954

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 954

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Arg Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 955

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 955

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ctgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 956

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 956

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Leu Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 957

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 957

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

gcgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 958

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 958

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ala Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 959

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 959

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 960

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 960

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 961

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 961

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gtgggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 962

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 962

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Val Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 963

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 963

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 964

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 964

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Lys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 965

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 965

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gaaggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 966

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 966

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Glu Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 967

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 967

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 968

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 968

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 969

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 969

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccct ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 970

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 970

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 971

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 971

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccac taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 972

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 972

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Thr Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 973
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 973

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ttacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc cgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 974

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 974

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Pro Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 975

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 975

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 976

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 976

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 977
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 977
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

gtttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 978

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 978

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Val Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 979

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 979

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 980

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 980

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 981

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 981

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tgttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 982

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 982

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Cys Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 983

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 983

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

atttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 984

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 984

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ile Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 985

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 985

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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atgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 986

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 986

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Met Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 987

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 987

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt tgcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 988

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 988

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 989

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 989

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccgg ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 990

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 990

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Gly Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 991

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 991

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gggccgcagt ttggttggta tgcgccggcg tttacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 992

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 992

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Phe Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 993

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 993

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 994

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 994

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Leu Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 995

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 995

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 996

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 996

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Val Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 997

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 997

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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 998

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 998

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Thr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 999

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 999

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgcgccggcg tgtacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1000

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1000

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Cys Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1001

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1001

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1002

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1002

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Asn Thr

20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1003

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1003

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1004

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1004

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Met Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1005
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1005

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1006

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1006

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Lys Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1007

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1007

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cataa 2295

<210> 1008

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1008

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1009

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1009

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1010

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1010

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1011
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1011
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tgtacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggcccgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1012

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1012

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Cys Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Pro Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1013

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1013

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1014

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1014

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1015

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1015

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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atgtgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1016

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1016

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Val Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1017

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1017

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgtg ctactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaggc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1018

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1018

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Gly Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1019

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1019

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1020

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1020

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1021

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1021

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctacaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1022

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1022

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1023

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1023

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1024

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1024

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1025

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1025

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1026

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1026

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1027

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1027

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1028

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1028

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Val Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1029

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1029

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ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg ttaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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gataaactgg ctagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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acgcaaacgg cgtaa 2295

<210> 1030

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1030

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Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1031

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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acgcaaacgg cgtaa 2295

<210> 1032

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1032

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Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1033

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1033

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1034
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1034
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1035

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1035

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1036

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1036

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1037
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1037

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cacgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccgcccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1038

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1038

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Thr Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Ala Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1039
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1039

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

aataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1040

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1040

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asn Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1041

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1041

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccta taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1042

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1042

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Tyr Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1043
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1043
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcacaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1044

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1044

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1045

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1045

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggtg tacgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcgttcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1046

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1046

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Cys Thr Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Phe Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1047

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1047

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1048

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1048

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1049

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1049

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gggccgcagt ttggttggta tgtgccggcg tacacctatg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac tgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1050

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1050

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Tyr Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1051

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1051

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gcggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1052

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1052

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Arg Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1053

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1053

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

atctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1054

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1054

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ile Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1055

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1055

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcagccg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattccattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt tgcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1056

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1056

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Pro Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1057

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1057

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gatagactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100

gtctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1058

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1058

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Arg Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Val Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1059

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1059

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttactt tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1060

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1060

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1061

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1061

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1062

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1062

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Cys Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1063

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1063

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1064

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1064

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1065

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1065

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaagccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt ttcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1066

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1066

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Ala Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Phe Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1067

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1067

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac caggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1068

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1068

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Gln Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1069

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1069

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaacac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1070

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1070

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Thr Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1071
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1071

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt tcacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1072

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1072

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1073

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1073

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgttaggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcgaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1074

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1074

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Arg Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Glu Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1075
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1075
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaagat gtacgagagc tttggccgta aatcgctgtg gttaacgccc 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1076

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1076

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1077

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1077

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tatggtgata aggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1078

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1078

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Tyr Gly Asp Lys Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1079

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1079

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg gcaacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1080

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1080

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Ala Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1081

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1081

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt aagggtgatc ttgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1082

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1082

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Lys Gly Asp Leu Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1083

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1083

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt aagggtgata atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaccagat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1084

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1084

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Lys Gly Asp Asn Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Pro Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1085

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1085

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg taccgttacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1086

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1086

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Arg
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1087
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1087

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccttgggt ggtggtgata cagtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1088
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1088
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Leu Gly Gly Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1089

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1089

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atcatgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1090

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1090

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp His Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1091

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1091

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

gcagcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1092

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1092

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Ala Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1093

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1093

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggtgtcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1094

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1094

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Cys Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1095

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1095

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg gggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1096

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1096

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Trp Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1097

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1097

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gaaggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1098

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1098

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1099

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1099

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ggcaccattt catggggatc caccgccggt gagggtgata cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1100

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1100

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1101
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1101

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tggggtgata ctgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1102

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1102

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Trp Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1103

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1103

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tggggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1104

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1104

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Trp Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1105

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1105

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tggggtgatt cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1106

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1106

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Trp Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1107
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1107
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gatggtgatc atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1108

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1108

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Asp Gly Asp His Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1109

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1109

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gatggtgata tggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1110

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1110

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Asp Gly Asp Met Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1111

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1111

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gatggtgatc ttgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1112

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1112

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asp Gly Asp Leu Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1113

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1113

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gagggtgata ctgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggtg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1114
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1114
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Val Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1115

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1115

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1116

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1116

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Trp Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1117

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1117

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gatggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1118

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1118

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Asp Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1119

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1119

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcgt atatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1120

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1120

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Tyr Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1121

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1121

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgata tggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1122

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1122

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Met Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1123

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1123

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt attggtgatc aggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atagcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1124

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1124

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Ile Gly Asp Gln Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Ser Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1125

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1125

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatc atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1126

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1126

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp His Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1127

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1127

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgtgg gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1128

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1128

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Trp Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1129

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1129

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt attggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggtgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1130

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1130

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Ile Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Val Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1131

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1131

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt aatggtgatc aggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1132

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1132

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asn Gly Asp Gln Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1133
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1133

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt aatggtgatg cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1134

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1134

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Asn Gly Asp Ala Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1135
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1135

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1136

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1136

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1137

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1137

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg ttgacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac caccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccgcccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac caggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaggc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1138

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1138

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Leu Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Thr Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Ala Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Gln Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Gly Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1139
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1139
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aatggtgatg ttgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctgcccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1140

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1140

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Asn Gly Asp Val Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Cys Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1141

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1141

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1142

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1142

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1143

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1143

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacacacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1144

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1144

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1145

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1145

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt aatggtgatt ctgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1146

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1146

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Asn Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1147

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1147

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg aggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1148

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1148

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Glu Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1149
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1149

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tatggtgatt tggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1150

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1150

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Tyr Gly Asp Leu Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1151
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1151

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatt ctgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1152

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1152

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1153

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1153

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt catggtgatg ctgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1154

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1154

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly His Gly Asp Ala Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1155
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1155
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cttggtgata tggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1156

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1156

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Leu Gly Asp Met Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1157

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1157

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt actggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1158

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1158

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Thr Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1159

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1159

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1160

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1160

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1161

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1161

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgataatt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1162

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1162

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Asn Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1163

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1163

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcagtttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1164

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1164

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ser Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1165

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1165

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1166

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1166

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Glu Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1167

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1167

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tccatttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1168

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1168

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe His Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1169

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1169

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatatgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1170

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1170

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Met Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1171

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1171

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccat atggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1172

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1172

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Tyr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1173

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1173

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcaat tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1174

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1174

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Gln Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1175

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1175

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact taaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1176

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1176

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1177

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1177

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tctatttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1178

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1178

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Tyr Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1179

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1179

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttctat 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1180

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1180

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Tyr Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1181

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1181

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1182

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1182

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1183

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1183

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgtgtat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1184

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1184

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Cys
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1185

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1185

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacatg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1186

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1186

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1187
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1187
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggccg tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1188

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1188

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Arg Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1189

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1189

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgaaatg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1190

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1190

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Lys Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1191

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1191

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgaggtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1192

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1192

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Arg Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1193

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1193

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1194

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1194

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1195

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1195

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1196

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1196

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1197

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1197

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1198

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1198

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1199
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1199

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1200
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1200
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1201

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1201

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1202

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1202

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1203

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1203

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1204

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1204

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1205

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1205

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1206

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1206

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1207

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1207

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ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1208

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1208

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1209

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1209

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1210

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1210

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1211

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1211

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1212

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1212

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Thr Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1213
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1213

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1214

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1214

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1215

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1215

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1216

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1216

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1217
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1217
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1218

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1218

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1219

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1219

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1220

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1220

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1221

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1221

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1222

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1222

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1223

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1223

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1224

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1224

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1225

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1225

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1226
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1226
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1227

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1227

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gtgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1228

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1228

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1229

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1229

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1230

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1230

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1231

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1231

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1232

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1232

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1233

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1233

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1234

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1234

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

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755 760

<210> 1235

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1235

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1236

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1236

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1237

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1237

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1238

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1238

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1239

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1239

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac agcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1240

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1240

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1241

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1241

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1242

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1242

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1243

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1243

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1244

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1244

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1245
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1245

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1246

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1246

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1247
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1247

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1248

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1248

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1249

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1249

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1250

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1250

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1251

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1251

agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1252

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1252

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1253

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1253

agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga tgagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1254

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1254

Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Glu Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1255

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1255

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1256

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1256

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1257

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1257

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcatt gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1258

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1258

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1259

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1259

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacatg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1260

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1260

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760
<210> 1261
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1261

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1262

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1262

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1263

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1263

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gggccgcagt ttggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggcaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtgatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagataaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1264

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1264

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1265

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1265

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1266

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1266

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1267

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1267

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ctgggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1268

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1268

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Leu Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1269

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1269

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgtggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1270

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1270

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1271

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1271

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cgtggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1272

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1272

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Arg Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1273

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1273

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1274

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1274

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser


    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys


        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His


            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe


                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1275

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1275

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1276

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1276

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1277
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1277

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctgtt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1278

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1278

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1279

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1279

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1280

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1280

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1281
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1281
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ttacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1282

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1282

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1283

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1283

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1284

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1284

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1285

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1285

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cagggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggt cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1286

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1286

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gln Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Ser Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1287

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1287

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1288
<211> 764
<212> PRT
<213> Artificial Sequence

<220
><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1288

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1289

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1289

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1290

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1290

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1291

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1291

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

gtttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1292

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1292

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Val Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1293

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1293

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgtcggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgtccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaagcg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1294

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1294

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Ser Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Ser
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Ser Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1295

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1295

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcgg 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gggggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1296

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1296

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Arg Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Gly Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1297

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1297

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg cacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttctctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1298

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1298

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala His Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1299

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1299

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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaaccgt 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggtaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1300

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1300

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Arg

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1301

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1301

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgtgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctattcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1302

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1302

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1303

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1303

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1304

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1304

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Leu Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1305

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1305

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatac ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1306

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1306

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Thr Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1307

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1307

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gggccgcagt ttggttgtta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1308

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1308

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Cys Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1309
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1309

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

aatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1310

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1310

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asn Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1311

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1311

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1312

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1312

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1313
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1313
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1314

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1314

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1315

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1315

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1316

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1316

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1317

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1317

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1318

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1318

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1319

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1319

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1320

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1320

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1321

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1321

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1322

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1322

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1323

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1323

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1324

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1324

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1325

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1325

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1326

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1326

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1327

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1327

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1328

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1328

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1329

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1329

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1330

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1330

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1331

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1331

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1332

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1332

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1333

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1333

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1334

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1334

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1335

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1335

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1336

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1336

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1337

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1337

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1338

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1338

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

```
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1339

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1339

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1340

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1340

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1341
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1341

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1342

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1342

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1343

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1343

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1344

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1344

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1345
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1345
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1346

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1346

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1347
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1347
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1348

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1348

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1349

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1349

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1350

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1350

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1351

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1351

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1352

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1352

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1353

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1353

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1354

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1354

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1355

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1355

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1356

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1356

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1357

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1357

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1358

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1358

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1359

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1359

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1360

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1360

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1361

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1361

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1362

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1362

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1363

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1363

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1364

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1364

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1365

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1365

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1366

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1366

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1367

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1367

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacggaccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1368

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1368

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1369

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1369

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1370
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1370
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp


    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr


        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln


            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu


                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1371

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1371

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1372

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1372

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1373
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1373

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1374

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1374

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1375
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1375

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1376

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1376

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

```
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1377

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1377

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1378

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1378

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1379
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1379
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1380

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1380

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1381

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1381

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1382

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1382

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1383

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1383

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1384

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1384

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1385

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1385

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1386

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1386

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1387

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1387

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1388

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1388

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1389

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1389

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1390

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1390

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1391

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1391

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1392

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1392

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1393

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1393

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1394

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1394

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1395
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1395
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1396

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1396

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1397

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1397

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1398

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1398

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1399

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1399

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ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1400

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1400

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1401

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1401

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1402

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1402

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1403

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1403

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1404

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1404

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1405

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1405

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1406

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1406

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1407
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1407

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1408

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1408

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1409

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1409

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1410

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1410

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1411
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1411
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1412

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1412

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1413

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1413

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1414

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1414

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1415

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1415

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1416

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1416

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1417

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1417

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1418

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1418

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1419

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1419

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1420

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1420

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1421

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1421

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1422

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1422

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1423
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1423

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1424
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1424

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40				45					

Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55				60					
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70				75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85				90					95			
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1425

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1425

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1426

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1426

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1427

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1427

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1428

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1428

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1429

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1429

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1430

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1430

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1431

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1431

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1432

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1432

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1433

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1433

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgtcatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1434

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1434

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Val Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1435

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1435

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1436

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1436

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1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1437
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1437

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1438

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1438

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1439

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1440

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1440

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1441
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1441
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1442

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1442

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1443
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1443
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1444

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1444

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1445

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1445

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1446

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1446

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1447

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1447

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1448

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1448

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1449

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1449

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1450
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1450
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1451

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1451

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1452

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1452

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1453

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1453

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1454

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1454

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1455

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1455

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1456

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1456

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1457

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1457

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1458

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1458

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1459

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1459

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tgggttgatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1460

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1460

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Leu Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1461

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1461

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1462

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1462

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1463

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1463

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1464

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1464

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
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225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1465

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1465

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1466

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1466

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1467

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1467

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ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1468

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1468

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1469
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1469

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1470

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1470

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1471
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1471

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1472

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1472

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1473

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1473

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1474

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1474

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1475
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1475
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1476

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1476

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1477

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1477

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1478

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1478

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1479

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1479

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ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1480

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1480

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
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225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1481

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1481

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1482

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1482

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1483

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1483

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1484

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1484

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1485
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1485

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1486

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1486

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1487
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1487

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1488

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1488

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1489

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1489

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1490

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1490

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1491
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1491
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1492

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1492

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1493

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1493

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1494

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1494

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
```

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1495
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1495
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1496

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1496

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1497

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1497

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1498

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1498

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1499

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1499

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1500

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1500

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1501

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1501

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1502

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1502

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1503

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1503

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1504

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1504

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1505

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1505

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1506

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1506

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1507

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1507

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1508

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1508

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1509

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1509

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgt ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1510

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1510

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Val Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1511

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1511

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1512

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1512

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1513

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1513

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1514

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1514

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1515

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1515

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1516

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1516

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1517

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1517

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1518

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1518

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1519
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1519

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1520

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1520

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1521

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1521

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1522

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1522

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1523
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1523
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1524

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1524

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1525

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1525

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1526

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1526

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1527

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1527

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1528

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1528

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1529

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1529

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1530

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1530

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1531

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1531

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1532

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1532

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1533

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1533

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1534

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1534

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1535
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1535

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1536
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1536

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10					15		
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20				25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40				45					

Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Pro	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1537

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1537

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

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acgcaaacgg cgtaa 2295

<210> 1538

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1538

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1539

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1539

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ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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acgcaaacgg cgtaa 2295

<210> 1540

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1540

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1541

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1541

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1542

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1542

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1543

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1543

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1544

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1544

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1545

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1545

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1546

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1546

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1547

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1547

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1548

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1548

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

```
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1549
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1549

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1550

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1550

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1551

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1551

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1552

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1552

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1553

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1553

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1554

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1554

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1555
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1555
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1556

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1556

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1557

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1557

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1558

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1558

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1559

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1559

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1560

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1560

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1561

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1561

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1562
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1562
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1563

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1563

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1564

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1564

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1565

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1565

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1566

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1566

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1567

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1567

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1568

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1568

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

```
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1569

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1569

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1570

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1570

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1571

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1571

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1572

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1572

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1573

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1573

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1574

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1574

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1575

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1575

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1576

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1576

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1577

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1577

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggctgt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1578

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1578

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Cys Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1579

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1579

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1580

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1580

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1581
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1581

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1582

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1582

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1583
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1583

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1584

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1584

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1585

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1585

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1586

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1586

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1587
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1587
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1588

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1588

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1589

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1589

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1590

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1590

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1591

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1591

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1592

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1592

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1593

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1593

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1594

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1594

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1595

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1595

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1596

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1596

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1597
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1597

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1598

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1598

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1599
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1599

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1600

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1600

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1601

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1601

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1602

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1602

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1603
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1603
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1604

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1604

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1605

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1605

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1606

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1606

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
```

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1607

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1607

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1608

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1608

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1609

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1609

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1610

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1610

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1611

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1611

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1612

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1612

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1613

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1613

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1614

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1614

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1615

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1615

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1616

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1616

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1617

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1617

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1618

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1618

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1619

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1619

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1620

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1620

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1621

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1621

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1622

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1622

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1623

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1623

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1624

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1624

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1625

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1625

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1626

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1626

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1627

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1627

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1628

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1628

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1629

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1629

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1630

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1630

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1631
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1631

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1632

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1632

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1633

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1633

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1634

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1634

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1635
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1635
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1636

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1636

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1637

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1637

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1638

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1638

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1639

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1639

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1640

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1640

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1641

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1641

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

aatgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1642

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1642

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asn Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1643

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1643

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1644

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1644

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1645

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1645

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1646

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1646

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1647
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1647

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1648
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1648

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1649

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1649

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1650

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1650

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1651

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1651

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1652

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1652

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1653

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1653

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1654

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1654

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1655

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1655

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1656

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1656

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1657

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1657

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1658

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1658

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1659

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1659

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1660

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1660

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
```

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1661
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1661

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1662

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1662

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1663

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1663

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1664

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1664

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1665

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1665

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1666

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1666

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1667
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1667
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1668

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1668

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1669

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1669

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1670

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1670

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1671

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1671

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1672

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1672

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1673

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1673

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1674
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1674
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1675

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1675

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1676

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1676

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1677

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1677

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggtg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1678

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1678

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Val Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1679

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1679

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1680

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1680

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

```
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1681

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1681

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1682

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1682

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1683

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1683

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1684

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1684

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1685

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1685

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1686

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1686

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1687

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1687

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1688

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1688

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1689

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1689

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1690

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1690

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1691

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1691

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1692

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1692

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1693
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1693

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1694

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1694

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1695
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1695

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1696

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1696

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1697

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1697

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1698

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1698

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1699
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1699
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1700

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1700

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1701

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1701

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1702

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1702

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1703

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1703

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1704
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1704

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1705

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1705

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1706

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1706

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1707

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1707

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1708

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1708

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1709
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1709

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1710

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1710

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1711
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1711

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1712

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1712

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

```
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1713

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1713

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actagtacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1714

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1714

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ser Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1715
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1715
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacga tgaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1716

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1716

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Met Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1717

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1717

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaatgga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1718

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1718

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Trp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1719

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1719

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatcgtt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1720

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1720

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Arg Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1721

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1721

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagat gtactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1722

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1722

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Met Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1723

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1723

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagcg ttactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1724

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1724

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Arg Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1725

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1725

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1726

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1726

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1727

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1727

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat cttgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1728

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1728

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Leu Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1729

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1729

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcgttgcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1730

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1730

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Val Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1731

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1731

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

ttggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1732

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1732

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Leu Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1733

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1733

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

cgtgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1734

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1734

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Arg Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1735

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1735

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1736

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1736

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Gly Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1737

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1737

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcaag taaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1738

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1738

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ser Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1739

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1739

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc tgatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1740

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1740

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1741

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1741

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1742

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1742

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1743
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1743

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagtta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1744

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1744

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Val Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1745

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1745

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gccatgcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1746

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1746

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly His Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1747
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1747
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagcaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1748

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1748

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1749

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1749

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

caagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1750

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1750

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Gln Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1751

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1751

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaaggtt tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1752

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1752

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Val Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1753

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1753

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gctgtgcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1754

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1754

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Cys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1755

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1755

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1756

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1756

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1757

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1757

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1758

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1758

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1759
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1759

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatatgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1760
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1760
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Met Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1761

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1761

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgcatct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1762

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1762

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala His

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1763

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1763

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaacgttt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1764

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1764

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Arg Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1765

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1765

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

cgtgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1766

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1766

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Arg Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1767

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1767

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1768

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1768

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1769

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1769

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ggggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1770

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1770

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1771

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1771

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1772

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1772

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Leu Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1773
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1773

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgctttgtt tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1774

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1774

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Cys Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1775

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1775

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1776

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1776

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Val Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1777
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1777
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1778

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1778

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1779
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1779
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta cccaagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1780

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1780

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Lys

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1781

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1781

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaatata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1782

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1782

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Tyr Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1783

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1783

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1784

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1784

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1785

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1785

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaacgta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1786
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1786
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1787

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1787

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaattta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1788

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1788

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Phe Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1789

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1789

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1790

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1790

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1791

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1791

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaatata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1792

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1792

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Tyr Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1793

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1793

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

attgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1794

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1794

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Ile Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1795

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1795

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1796

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1796

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1797

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1797

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1798

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1798

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1799

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1799

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1800

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1800

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1801

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1801

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaacgta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1802

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1802

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1803

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1803

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

caagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1804

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1804

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Gln Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1805
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1805

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1806

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1806

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1807
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1807

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcattttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1808

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1808

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ile Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1809

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1809

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatgttt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1810

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1810

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1811
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1811
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatagtt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1812

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1812

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Ser Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1813

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1813

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaagga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1814

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1814

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1815

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1815

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct ggaaatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1816

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1816

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Glu Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1817

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1817

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccac aaacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1818

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1818

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Thr Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1819

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1819

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgcag ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccca 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1820

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1820

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Ser Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Pro Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1821
<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1821

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagctata gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1822

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1822

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Tyr Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1823
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1823

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcaaaa gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1824

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1824

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

355 360 365

Lys Trp Tyr Ser Lys Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1825

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1825

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccaaaga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1826

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1826

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Lys Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1827
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1827
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1828

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1828

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1829

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1829

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taaagcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcaac aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1830

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1830

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Lys Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Thr Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1831

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1831

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattggtaac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1832

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1832

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Gly Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1833

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1833

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgcaaac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1834

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1834

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Ala Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1835

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1835

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1836

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1836

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1837

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1837

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattaataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1838

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1838

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asn Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1839

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1839

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgaaac agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1840

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1840

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Lys Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1841

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1841

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattcataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1842

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1842

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile His Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1843

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1843

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatgc aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1844

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1844

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Ala Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1845

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1845

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtaaa 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1846

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1846

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Lys Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1847

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1847

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccaggga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1848

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1848

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Arg Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1849

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1849

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattaggaac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1850

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1850

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Arg Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1851

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1851

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcgtcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1852

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1852

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg Arg Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1853

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1853

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcagt 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattcaaaac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1854

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1854

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Ser Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Gln Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1855
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1855

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1856

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1856

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1857

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1857

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattagtaac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1858

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1858

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Ser Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1859
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1859
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1860

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1860

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1861

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1861

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcgaaagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1862

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1862

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Glu Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1863

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1863

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga cagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1864

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1864

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1865

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1865

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcccattcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1866

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1866

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Pro Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1867

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1867

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt ctgtagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1868

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1868

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Cys Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1869

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1869

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgaattcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1870

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1870

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Glu Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1871
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1871

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccatgggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1872
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1872
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Met Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1873

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1873

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga cagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1874

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1874

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1875

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1875

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1876

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1876

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1877

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1877

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgcaggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg tcgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1878

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1878

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Val Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1879

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1879

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1880

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1880

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1881

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1881

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggaaaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1882

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1882

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Lys Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1883

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1883

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc cacccttggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1884

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1884

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Leu Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1885
<211> 2295
<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1885

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

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ttctctgaca gcaccagcga agttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1886

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1886

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Val Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1887

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1887

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aatggataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1888

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1888

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Met Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1889

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1889

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcaaattcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1890

<211> 764

<212> PRT

<213> Artificial Sequence

<220

><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1890

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Lys Phe

245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr

370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1891
<211> 2295
<212> DNA
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1891
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctga cagcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1892

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1892

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1893

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1893

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tccgtttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1894

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1894

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Arg Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1895

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1895

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgttggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1896

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1896

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Val Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly

355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln

420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro

485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760

<210> 1897

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1897

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggcgta ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1898
<211> 764
<212> PRT
<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1898
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Arg Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala

500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr

545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1899

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1899

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcagtagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1900

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1900

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Ser Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1901

<211> 2295

<212> DNA

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1901

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900

ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080

gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140

gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260

gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380

ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcagtagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1902

<211> 764

<212> PRT

<213> Artificial Sequence

<220><223> Penicillin-G Acylates Variant from K. citrophila

<400> 1902

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly

465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp

530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala

565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln

580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile

610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu

625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn

645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln

660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

690 695 700

Ser Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys

705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu

725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr

740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

755 760